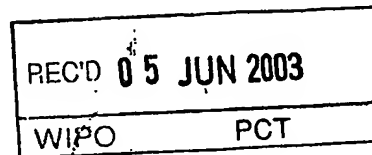# Kongeriget Danmark

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Applicant:
(Name and address)
   Novozymes A/S
Krogshøjvej 36
2880 Bagsværd
Denmark

Title: Improved Bacillus Host Cell

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This is to certify that the attached documents are exact copies of the above mentioned patent application as originally filed.

PRIORITY DOCUMENT

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Patent- og Varemærkestyrelsen
Økonomi- og Erhvervsministeriet

29 April 2003

Pia Høybye-Olsen

PATENT- OG VAREMÆRKESTYRELSEN

●

TITLE: Improved Bacillus Host Cell

TECHNICAL FIELD

Bacillus sp. are attractive hosts for the production of heterologous proteins due their ability to
secrete proteins directly into the culture medium. They have a high capacity for protein
secretion, are genetically highly amenable, nonpathogenic and free of endotoxins, and
consequently a large variety of proteins from different organisms have been efficiently
produced and secreted in *Bacillus sp. i.e.* In *Bacillus licheniformis.*

In the highly competitive biotech industry, even slightly improved *Bacillus* host cells are in
demand, which may provide more attractive production systems, or may even just be
alternative production systems.

BACKGROUND

Many industrial products of commercial interest can be produced biologically in *Bacillus sp.*
host cells e.g. heterologous polypeptides, amino acids, carbohydrates etc. Some of these
products are sold as process aids, intermediates, or even end-products in the food and feed
industries as well as in the pharmaceutical industry. There are increasingly strict regulations
that must be complied with when producing such products in microbial production hosts for
sale in these industries, for instance the presence of bacterial spores in the products is seen
as a problem. When producing in *Bacillus licheniformis* it is thus desirable to ensure that the
host cell is not capable of forming spores.

SUMMARY

A problem to be solved by the present invention is how to obtain a *Bacillus licheniformis* host
cell incapable of forming spores, or how to impair the sporulation process of said cell. The
present invention provides a solution to the problem by providing a *Bacillus licheniformis* host
cell which has a reduced capacity to produce one or more polypeptide(s) involved in
sporulation.

Accordingly, in a first aspect the invention relates to a *Bacillus licheniformis* mutant host cell
derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or
more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least
80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 129, preferably
at least 85% identical, more preferably at least 90% identical, still more preferably at least
95% identical, and most preferably at least 97% identical to one or more of the polypeptides
shown in SEQ ID NO's: 2 to 129, wherein the mutant host cell expresses at least 5% less of
the one or more polypeptide(s) involved in sporulation than the parent host cell, when they
are cultivated under comparable conditions. Preferably the mutant host cell expresses at

least 10% less, more preferably at least 20% less, still more preferably at least 30% less, even more preferably at least 40% less, yet more preferably at least 50% less, or at least 60% less, or at least 70% less, or at least 80%, or most preferably at least 90% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions. Most preferably the mutant host cell expresses absolutely nothing of the one or more polypeptide(s) involved in sporulation.

Comparable conditions of cultivation must be used in order to compare the expression level of the one or more polypeptide(s) involved in sporulation in a mutant host cell of the invention with that in a parent host cell. They are cultivated separately under identical conditions in identical setups, of course allowing for the usual standard deviations of the operating parameters normally associated with growth experiments, such as temperature control etc. The quantification of the expression level of the one or more polypeptide(s) is done by standard text-book assay techniques as known in the art e.g. mRNA quantification or immuno-based assays.

In a second aspect the invention relates to a process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in the previous aspect in a suitable medium, whereby the said product is produced.

Finally, an aspect of the invention relates to a use of a *Bacillus licheniformis* mutant host cell as defined in the first aspect for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced.

DEFINITIONS

Nucleic acid construct: When used herein, the term "nucleic acid construct" means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or which has been modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature. The term nucleic acid construct is synonymous with the term "expression cassette" when the nucleic acid construct contains the control sequences required for expression of a coding sequence of the present invention.

Control sequence: The term "control sequences" is defined herein to include all components, which are necessary or advantageous for the expression of a polypeptide of the present invention. Each control sequence may be native or foreign to the nucleotide sequence encoding the polypeptide. Such control sequences include, but are not limited to, a leader,

polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control

5 sequences with the coding region of the nucleotide sequence encoding a polypeptide.

Operably linked: The term "operably linked" is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to the coding sequence of the DNA sequence such that the control sequence directs the expression of a polypeptide.

10

Coding sequence: When used herein the term "coding sequence" is intended to cover a nucleotide sequence, which directly specifies the amino acid sequence of its protein product. The boundaries of the coding sequence are generally determined by an open reading frame, which usually begins with the ATG start codon. The coding sequence typically include DNA,

15 cDNA, and recombinant nucleotide sequences.

Expression: In the present context, the term "expression" includes any step involved in the production of the polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

20

Expression vector: In the present context, the term "expression vector" covers a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of the invention, and which is operably linked to additional segments that provide for its transcription.

25

DETAILED DISCLOSURE

A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the

30 polypeptides shown in SEQ ID NO's: 2 to 129, wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions.

The term "parent host cell" in the context of the present invention means a cell which is

35 genetically identical, or isogenic, to the progeny mutant or mutant cell of the present invention, except for the mutated one or more gene(s) encoding one or more polypeptide(s) involved in sporulation in said mutant.

The degree of identity, or %-identity of polypeptide sequences can suitably be investigated by aligning the sequences using a computer program known in the art, such as "GAP" provided in the GCG program package (Program Manual for the Wisconsin Package,
5   Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711)(Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-453). Using GAP with the following settings for DNA sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3".

10   An object of the present invention is to provide a culture medium free of bacterial spores so as to reduce the product purification to a minimum, and to comply with regulatory requirements. This may be done according to the invention by reducing or even completely abolishing the expression of one or more gene(s) encoding a native polypeptide(s) involved in sporulation via mutagenisation of that (those) gene(s). One of the very well-known method
15   of ensuring that a gene is not expressed into an active polypeptide within a cell is simply to delete or partially delete the encoding gene. Many techniques have been described in the art on how to specifically delete or partially delete one or more gene(s) in the genome of a cell, and certainly from the genome of a *Bacillus licheniformis* cell (see e.g. Novozymes A/S WO 01/90393, Novozymes A/S WO 02/00907). Accordingly, a preferred embodiment of the
20   present invention relates to a host cell of the first aspect, which is mutated by a partial or complete deletion of the one or more gene(s) encoding the one or more polypeptide(s) involved in sporulation.

A preferred embodiment of the present invention relates to a host cell of the first aspect,
25   which is mutated in two or more genes encoding two or more polypeptides involved in sporulation.

The product of interest to be produced by the mutant host cell of the first aspect may be one or more polypeptide(s) encoded by one or more heterologous gene(s). Consequently, a
30   preferred embodiment of the present invention relates to a host cell of the first aspect, which comprises one or more heterologous gene(s) encoding one or more heterologous polypeptide(s).

In the industrial production of polypeptides it is of interest to achieve a product yield as high
35   as possible. One way to increase the yield is to increase the copy number of a gene encoding a polypeptide of interest. This can be done by placing the gene on a high copy number plasmid. However, plasmids are unstable and are often lost from the host cells if

there is no selective pressure during the cultivation of the host cells. Another way to increase the copy number of the gene of interest is to integrate it into the host cell chromosome in multiple copies. Integration of two genes has been described in WO 91/09129 and WO 94/14968 (Novozymes A/S) the content of which is hereby incorporated by reference. A

5   preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) is present in at least two copies, preferably at least 4 copies, and most preferably at least 6 copies. In another embodiment the heterologous gene(s) is present in at least ten copies. If carried on a plasmid the gene(s) may be present in several hundred copies per cell, so in a still further embodiment of the present invention

10   the heterologous gene(s) is present in at least 100 copies.

Integration of two genes closely spaced in anti-parallel tandem to achieve better stability has been described in WO 99/41358 (Novozymes A/S) the content of which is hereby incorporated by reference, as well as the stable chromosomal multi-copy integration of genes

15   described in WO 02/00907 (Novozymes A/S) the content of which is incorporated herein by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are stably integrated into the genome of the cell.

Selection of chromosomal integrant has for convenience resulted in the use of selectable

20   markers such as antibiotic resistance markers. However it is desirable if possible to avoid the use of antibiotic marker genes. WO 01/90393 discloses a method for the integration of a gene in the chromosome of a host cell without leaving antibiotic resistance markers behind in the strain, the content of which is hereby incorporated by reference A preferred embodiment of the present invention relates to a host cell of the first aspect wherein the heterologous

25   gene(s) is integrated into the genome of the cell without leaving any antibiotic resistance marker gene(s) at the site of integration.

The present invention also relates to nucleic acid constructs comprising a nucleotide sequence encoding a product of interest, which may be operably linked to one or more

30   control sequences that direct the expression of the coding sequence in a suitable host cell under conditions compatible with the control sequences.

A nucleotide sequence encoding a polypeptide of interest may be manipulated in a variety of ways to provide for expression of the polypeptide. Manipulation of the nucleotide sequence

35   prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying nucleotide sequences utilizing recombinant DNA methods are well known in the art.

Other ways of increasing the product yield would be to increase promoter activity of the specific promoter regulating the expression of a specific gene of interest. Also a more general increase in the activity of several promoters at the same time could lead to an improved product yield. The control sequence may be an appropriate promoter sequence, a nucleotide sequence which is recognized by a host cell for expression of the nucleotide sequence. The promoter sequence contains transcriptional control sequences, which mediate the expression of the polypeptide. The promoter may be any nucleotide sequence which shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

Examples of suitable promoters for directing the transcription of the nucleic acid constructs of the present invention, especially in a bacterial host cell, are the promoters obtained from the E. coli lac operon, Streptomyces coelicolor agarase gene (dagA), Bacillus subtilis levansucrase gene (sacB), Bacillus licheniformis alpha-amylase gene (amyL), Bacillus stearothermophilus maltogenic amylase gene (amyM), Bacillus amyloliquefaciens alpha-amylase gene (amyQ), Bacillus licheniformis penicillinase gene (penP), Bacillus subtilis xylA and xylB genes, and prokaryotic beta-lactamase gene (Villa-Kamaroff et al., 1978, Proceedings of the National Academy of Sciences USA 75: 3727-3731), as well as the tac promoter (DeBoer et al., 1983, Proceedings of the National Academy of Sciences USA 80: 21-25). Further promoters are described in "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242: 74-94; and in Sambrook et al., 1989, supra.

Other useful promoters are described in WO 93/10249, WO 98/07846, and WO 99/43835 (Novozymes A/S) the contents of which are incorporated fully herein by reference. A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are transcribed from a heterologous promoter or from an artificial promoter.

The control sequence may also be a suitable transcription terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleotide sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice may be used in the present invention.

The control sequence may also be a suitable leader sequence, a nontranslated region of an mRNA which is important for translation by the host cell. The leader sequence is operably

linked to the 5' terminus of the nucleotide sequence encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used in the present invention.

The control sequence may also be a polyadenylation sequence, a sequence operably linked
5 to the 3' terminus of the nucleotide sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the present invention.

10 The control sequence may also be a signal peptide coding region that codes for an amino acid sequence linked to the amino terminus of a polypeptide and directs the encoded polypeptide into the cell's secretory pathway. The 5' end of the coding sequence of the nucleotide sequence may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted
15 polypeptide. Alternatively, the 5' end of the coding sequence may contain a signal peptide coding region which is foreign to the coding sequence. The foreign signal peptide coding region may be required where the coding sequence does not naturally contain a signal peptide coding region. Alternatively, the foreign signal peptide coding region may simply replace the natural signal peptide coding region in order to enhance secretion of the
20 polypeptide. However, any signal peptide coding region which directs the expressed polypeptide into the secretory pathway of a host cell of choice may be used in the present invention.

Effective signal peptide coding regions for bacterial host cells are the signal peptide coding
25 regions obtained from the genes for Bacillus NCIB 11837 maltogenic amylase, Bacillus stearothermophilus alpha-amylase, Bacillus licheniformis subtilisin, Bacillus licheniformis beta-lactamase, Bacillus stearothermophilus neutral proteases (nprT, nprS, nprM), and Bacillus subtilis prsA. Further signal peptides are described by Simonen and Palva, 1993, Microbiological Reviews 57: 109-137.

30
The control sequence may also be a propeptide coding region that codes for an amino acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to a mature active polypeptide by catalytic or
35 autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding region may be obtained from the genes for Bacillus subtilis alkaline protease (aprE), Bacillus

subtilis neutral protease (nprT), Saccharomyces cerevisiae alpha-factor, Rhizomucor miehei aspartic proteinase, and Myceliophthora thermophila laccase (WO 95/33836).

Where both signal peptide and propeptide regions are present at the amino terminus of a polypeptide, the propeptide region is positioned next to the amino terminus of a polypeptide and the signal peptide region is positioned next to the amino terminus of the propeptide region.

It may also be desirable to add regulatory sequences which allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory systems in prokaryotic systems include the lac, tac, and trp operator systems. In yeast, the ADH2 system or GAL1 system may be used. In eukaryotic systems, these include the dihydrofolate reductase gene which is amplified in the presence of methotrexate, and the metallothionein genes which are amplified with heavy metals. In these cases, the nucleotide sequence encoding the polypeptide would be operably linked with the regulatory sequence.

The present invention also relates to recombinant expression vectors comprising the nucleic acid construct of the invention. The various nucleotide and control sequences described above may be joined together to produce a recombinant expression vector which may include one or more convenient restriction sites to allow for insertion or substitution of the nucleotide sequence encoding the polypeptide at such sites. Alternatively, the nucleotide sequence of the present invention may be expressed by inserting the nucleotide sequence or a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

The recombinant expression vector may be any vector (e.g., a plasmid or virus) which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the nucleotide sequence. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids.

The vector may be an autonomously replicating vector, i.e., a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication,

e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome.

The vector may contain any means for assuring self-replication. Alternatively, the vector may
5   be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon may be used.

10   The vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

15   Examples of bacterial selectable markers are the dal genes from Bacillus subtilis or Bacillus licheniformis, or markers which confer antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracycline resistance.

The vectors of the present invention preferably contain an element(s) that permits stable
20   integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

For integration into the host cell genome, the vector may rely on the nucleotide sequence encoding the polypeptide or any other element of the vector for stable integration of the
25   vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleotide sequences for directing integration by homologous recombination into the genome of the host cell. The additional nucleotide sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the
30   integrational elements should preferably contain a sufficient number of nucleotides, such as 100 to 1,500 base pairs, preferably 400 to 1,500 base pairs, and most preferably 800 to 1,500 base pairs, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell.
35   Furthermore, the integrational elements may be non-encoding or encoding nucleotide sequences. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in E. coli, and pUB110, pE194, pTA1060, and pAMß1 permitting replication in Bacillus. The origin of replication may be one having a mutation which makes its functioning temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, Proceedings of the National Academy of Sciences USA 75: 1433).

More than one copy of a nucleotide sequence of the present invention may be inserted into the host cell to increase production of the gene product. An increase in the copy number of the nucleotide sequence can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the nucleotide sequence where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the nucleotide sequence, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook et al., 1989, supra).

The introduction of a vector into a bacterial host cell may, for instance, be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, Molecular General Genetics 168: 111-115), using competent cells (see, e.g., Young and Spizizin, 1961, Journal of Bacteriology 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, Journal of Molecular Biology 56: 209-221), electroporation (see, e.g., Shigekawa and Dower, 1988, Biotechniques 6: 742-751), or conjugation (see, e.g., Koehler and Thorne, 1987, Journal of Bacteriology 169: 5771-5278).

A preferred embodiment of the present invention relates to a host cell of the first aspect, wherein the heterologous gene(s) are comprised in an operon, preferably a polycistronic operon. The term "operon" in the context of the present invention means a polynucleotide comprising several genes that are clustered and perhaps even transcribed together into a polycistronic mRNA, e.g. genes coding for the enzymes of a metabolic pathway. The transcription of an operon may be initiated at a promoter region and controlled by a neighboring regulatory gene, which encodes a regulatory protein, which in turn binds to the operator sequence in the operon to respectively inhibit or enhance the transcription. The

gene or the operon can be carried on a suitable plasmid that can be stably maintained, e.g. capable of stable autonomous replication in the host cell (the choice of plasmid will typically depend on the compatibility of the plasmid with the host cell into which the plasmid is to be introduced) or it can be carried on the chromosome of the host. The said gene may be

5 endogenous to the host cell in which case the product of interest is a protein naturally produced by the host cell and in most cases the gene will be in it normal position on the chromosome. If the gene encoding the product of interest is an exogenous gene, the gene could either be carried on a suitable plasmid or it could be integrated on the host chromosome. In one embodiment of the invention the eubacterium is a recombinant

10 eubacterium. Also the product of interest may in another embodiment be a recombinant protein.

The product of interest is any gene product or product of a metabolic pathway which is industrially useful and which can be produced in a bacterial cell such as a B. licheniformis.

15

In one preferred embodiment, the heterologous polypeptide(s) is an antimicrobial peptide, or a fusion peptide comprising a peptide part which in its native form has antimicrobial activity.

In another preferred embodiment, the heterologous polypeptide(s) has biosynthetic activity

20 and produces a compound or an intermediate of interest.

Yet another embodiment relates to a host cell of the first aspect, wherein the compound or intermediate of interest comprises vitamins, amino acids, antibiotics, carbohydrates, or surfactants, and preferably the carbohydrates comprise hyaluronic acid.

25

In one embodiment the heterologous polypeptide(s) is an enzyme, particularly the enzyme is an enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6). Preferably the enzyme is an enzyme with an activity selected

30 from the group consisting of aminopeptidase, amylase, amyloglucosidase, mannanase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase,

35 phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, or xylanase. Preferably the enzyme is an amylase or a mannanase.

A second aspect of the invention relates to a process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in the first aspect of the invention in a suitable medium, whereby the said product is produced. One embodiment relates to a process of the second aspect,

5   further comprising isolating or purifying the product of interest. Suitable media for the cultivation is described below as well as methods for the purification or isolation of the produced product which is an optional additional step to the process of the present invention.

In the production methods of the present invention, the cells are cultivated in a nutrient

10   medium suitable for production of the polypeptide using methods known in the art. For example, the cell may be cultivated by shake flask cultivation, small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the polypeptide to be expressed and/or isolated. The cultivation takes place in a

15   suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (*e.g.*, in catalogues of the American Type Culture Collection). If the polypeptide is secreted into the nutrient medium, the polypeptide can be recovered directly from the medium. If the polypeptide is not secreted, it can be

20   recovered from cell lysates.

The medium used to culture the cells may be any conventional medium suitable for growing the host cells, such as minimal or complex media containing appropriate supplements. Suit-able media are available from commercial suppliers or may be prepared according to

25   published recipes (e.g. in catalogues of the American Type Culture Collection). The media are prepared using procedures known in the art (see, *e.g.*, references for bacteria and yeast; Bennett, J.W. and LaSure, L., editors, *More Gene Manipulations in Fungi*, Academic Press, CA, 1991).

30   The polypeptides may be detected using methods known in the art that are specific for the polypeptides. These detection methods may include use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, an enzyme assay may be used to determine the activity of the polypeptide as described herein.

35   The resulting polypeptide may be recovered by methods known in the art. For example, the polypeptide may be recovered from the nutrient medium by conventional procedures

including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation.

The polypeptides of the present invention may be purified by a variety of procedures known
5   in the art including, but not limited to, chromatography (*e.g.*, ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (*e.g.*, preparative isoelectric focusing), differential solubility (*e.g.*, ammonium sulfate precipitation), SDS-PAGE, or extraction (see, *e.g.*, *Protein Purification*, J.-C. Janson and Lars Ryden, editors, VCH Publishers, New York, 1989).

10

A third aspect of the present invention relates to the use of a *Bacillus licheniformis* mutant host cell as defined in the first aspect for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced, and optionally isolating or purifying the produced product.

15

CLAIMS

1. A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 129, wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions.

2. The host cell according to claim 1, which is mutated by a partial or complete deletion of the one or more gene(s) encoding the one or more polypeptide(s) involved in sporulation.

3. The host cell according to any of claims 1 – 2, which is mutated in two or more genes encoding two or more polypeptides involved in sporulation.

5. The host cell according to any of claims 1 – 4, which comprises one or more heterologous gene(s) encoding one or more heterologous polypeptide(s).

6. The host cell according to claim 5, wherein the heterologous gene(s) is present in at least two copies.

7. The host cell according to claim 5 or 6, wherein the heterologous gene(s) are stably integrated into the genome of the cell.

8. The host cell according to any of claims 5 - 7, wherein the heterologous gene(s) is integrated into the genome of the cell without leaving any antibiotic resistance marker genes at the site of integration.

9. The host cell according to any of claims 5 - 8, wherein the heterologous gene(s) are transcribed from a heterologous promoter or from an artificial promoter.

10. The host cell according to any of claim 5 – 9, wherein the heterologous gene(s) are comprised in an operon, preferably a polycistronic operon.

11. The host cell according to any of claims 5 – 10, wherein the heterologous polypeptide(s) is an antimicrobial peptide, or a fusion peptide comprising a peptide part which in its native form has antimicrobial activity.

12. The host cell according to any of claims 5 – 10, wherein the heterologous polypeptide(s) has biosynthetic activity and produces a compound or an intermediate of interest.

13. The host cell according to claim 12, wherein the compound or intermediate of interest comprises vitamins, amino acids, antibiotics, carbohydrates, or surfactants.

14. The host cell according to claim 13, wherein the carbohydrates comprise hyaluronic acid.

15. The host cell according to any of claims 5 – 10, wherein the heterologous polypeptide(s) is an enzyme, preferably a secreted enzyme.

16. The host cell according to claim 15, wherein the enzyme Is Is an enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (EC 1), transferases (EC 2), hydrolases (EC 3), lyases (EC 4), isomerases (EC 5), and ligases (EC 6).

17. The host cell according to claim 16, wherein the enzyme Is an enzyme with an activity selected from the group of enzyme activities consisting of aminopeptidase, amylase, amyloglucosidase, mannanase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, galactosidase, beta-galactosidase, glucoamylase, glucose oxidase, glucosidase, haloperoxidase, hemicellulase, invertase, isomerase, laccase, ligase, lipase, lyase, mannosidase, oxidase, pectinase, peroxidase, phytase, phenoloxidase, polyphenoloxidase, protease, ribonuclease, transferase, transglutaminase, and xylanase.

18. The host cell according to claim 17, wherein the enzyme Is an amylase or a mannanase.

19. A process for producing at least one product of interest in a *Bacillus licheniformis* mutant host cell, comprising cultivating a *B.licheniformis* mutant host cell as defined in any of the claims 1 - 18 in a suitable medium, whereby the said product is produced.

20. The process according to claim 19, further comprising isolating or purifying the product of interest.

21. A use of a *Bacillus licheniformis* mutant host cell as definde in any of the claims 1 - 18 for producing at least one product of interest comprising cultivating the mutant host cell in a suitable medium whereby the said product is produced.

22. The use according to claim 21 further comprising isolating or purifying the product of interest.

ABSTRACT

TITLE: Improved Bacillus Host Cell.

A *Bacillus licheniformis* mutant host cell derived from a parent *B. licheniformis* host cell, which mutant host cell is mutated in one or more gene(s) encoding one or more

5   polypeptide(s) involved in sporulation which is at least 80% identical to one or more of the polypeptides shown in SEQ ID NO's: 2 to 129, wherein the mutant host cell expresses at least 5% less of the one or more polypeptide(s) involved in sporulation than the parent host cell, when they are cultivated under comparable conditions.

SEQUENCE LISTING

<110> Novozymes A/S

Jørgensen, Steen Troels

Olesen, Peter Bjarke

Andersen, Jens Tønne

Rasmussen, Michael Dolberg

<120> Improved Bacillus Host Cell

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<160> 129

<170> PatentIn version 3.1

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120                 125                 130                 135

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Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln Lys Lys Gly Phe Ile
65              70              75                  80

Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro Leu Ser Lys Thr Asn
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Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile Ser Thr Phe His Gly
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Tyr Glu Val Thr Met Lys Glu Phe Gln Gln Gln Leu His Arg Asp Leu
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ccg ccg act cgg ctg ttt gga tat aac gga gtt tat ccc ggc cct acc      677
Pro Pro Thr Arg Leu Phe Gly Tyr Asn Gly Val Tyr Pro Gly Pro Thr
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Phe Glu Val Gln Lys His Glu Lys Val Ala Val Lys Trp Leu Asn Lys
60              65              70              75

ctt ccg gat cgc cat ttt ctc ccc gtc gac cat acg ctt cac gat gac      773
Leu Pro Asp Arg His Phe Leu Pro Val Asp His Thr Leu His Asp Asp
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ggc cat cac gaa cat gaa gtg aag acg gtc gtt cat ttg cac gga ggc      821
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140             145             150             155

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380             385                 390                 395

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Thr Asp Val Arg His Gln
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            15                  20                  25

att gtg ccg cat att cat ccg cag cat ata aca aat gtg cat cat aag      629
Ile Val Pro His Ile His Pro Gln His Ile Thr Asn Val His His Lys
        30                  35                  40

cat ttc cag cat gtg cat caa tat cca cac act tat tct agt tac gat      677
His Phe Gln His Val His Gln Tyr Pro His Thr Tyr Ser Ser Tyr Asp
    45                  50                  55
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Page 8

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             15                  20                  25

cct tcg caa aag cca acc agt att tta ggc ggt tgg att atc aat cat         629
Pro Ser Gln Lys Pro Thr Ser Ile Leu Gly Gly Trp Ile Ile Asn His
             30                  35                  40

aag tat gac gct gaa aaa atc gga aaa acc gtg gaa att gaa ggg aca         677
Lys Tyr Asp Ala Glu Lys Ile Gly Lys Thr Val Glu Ile Glu Gly Thr
             45                  50                  55

tat gat atc aac gtc tgg tat tca tat gcg gac aac acc aaa acc gaa         725
Tyr Asp Ile Asn Val Trp Tyr Ser Tyr Ala Asp Asn Thr Lys Thr Glu
60                  65                  70                  75

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                 80                  85                  90

cgc gac aaa aat tac tta gat gat gaa cac gaa gtc att gcg aaa gtg         821
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Lys Val Val Val Gln Ala Glu Arg Glu Phe Leu Ala Glu Val Val Gly
    125                 130                 135

gag acg aag gtc gtc gtt gag gtc aat tct gat tgg acg gaa agc gat        965
Glu Thr Lys Val Val Val Glu Val Asn Ser Asp Trp Thr Glu Ser Asp
140                 145                 150                 155

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                 160                 165                 170
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Page 10

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acgagcaggg acggaggatc aagcgaaaga attccgatgt gcggggttcc ttatcattcc    1366

tgctcttcgt atatcgaaca gctcattaaa aaaggctata aagtcgcgat ctgtgaacag    1426

gtggaggacc ctaaatcggc caaaggagtc gtcaaaaggg aagtcgtgca gctgatcaca    1486

cccggcaccg tgatggacgg caaagggatt catgaaaatg aaaacaactt tatcgcctct    1546

gtc                                                                  1549
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<210> 8

<211> 182

<212> PRT

<213> Bacillus licheniformis

<400> 8

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Met Ser Glu Tyr Arg Glu Ile Ile Thr Lys Ala Val Val Ala Lys Gly
1               5                   10                  15

Arg Lys Phe Thr Gln Ser Thr His Thr Ile Ser Pro Ser Gln Lys Pro
            20                  25                  30

Thr Ser Ile Leu Gly Gly Trp Ile Ile Asn His Lys Tyr Asp Ala Glu
        35                  40                  45

Lys Ile Gly Lys Thr Val Glu Ile Glu Gly Thr Tyr Asp Ile Asn Val
    50                  55                  60

Trp Tyr Ser Tyr Ala Asp Asn Thr Lys Thr Glu Val Val Thr Glu Arg
65                  70                  75                  80

Val Ser Tyr Val Asp Val Ile Lys Leu Arg Tyr Arg Asp Lys Asn Tyr
                85                  90                  95

Leu Asp Asp Glu His Glu Val Ile Ala Lys Val Leu Gln Gln Pro Asn
            100                 105                 110

Cys Leu Glu Val Thr Ile Ser Pro Asn Gly Asn Lys Val Val Val Gln
            115                 120                 125
```

```
Ala Glu Arg Glu Phe Leu Ala Glu Val Val Gly Glu Thr Lys Val Val
    130                 135             140
```

```
Val Glu Val Asn Ser Asp Trp Thr Glu Ser Asp Glu Glu Glu Ala Trp
145             150                 155                 160
```

```
Glu Glu Glu Leu Asp Glu Glu Leu Glu Asp Ile Asn Pro Glu Phe Leu
              165             170             175
```

```
Val Gly Asp Pro Glu Glu
              180
```

<210> 9

<211> 1477

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(974)

<223>

<400> 9
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gtatgttgaa atgtcatgaa tcaaaaagag cagcatagac gactgctctt ttctaacgtc      60

gcaatttcat tttcaaataa agacgatgag atgagcaggt ctcggccttc tctcattgtt     120

tctttattct aacataaggt caaatcgcaa gtaaaacgat cataaggctt gaaagcgagc     180

gaatgttcca tgtgaaacag tgtcagtcga gaaaccccga tttttcttta ttttctttc     240

tcgcctttct gatcagcaac aatataatca aaactgcgac cagaagcgtc acgcgaagcc     300

ctccgctcaa aaatagaaaa aagtccttca acatatccaa cacattgatc acctctcact     360

gttgtcactt agatgcaaaa atcccgtatt atttgacttc ccctttccaa aacggtctaa     420

aacgtccctc agattcttct taacctttag acggtaatgg gcatatgctg actaagaaaa     480

agcaataaag gagaatatga atg aca aca aaa aca ttg gct tgg cat gaa acg     533
                        Met Thr Thr Lys Thr Leu Ala Trp His Glu Thr
                        1               5                   10
```

```
ttg gag ttg cat gaa cta atc gcg gca cag tct gtc gga ttg gtg aag     581
Leu Glu Leu His Glu Leu Ile Ala Ala Gln Ser Val Gly Leu Val Lys
            15                  20                  25
```

```
atc aag aaa agc atg aag aaa atc agc gac cct cag tta aga cag ctt     629
Ile Lys Lys Ser Met Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu
            30                  35                  40
```

```
tac agc gtg tca gca aaa gca ttg gag caa aat tta aga gag ctt ctt     677
Tyr Ser Val Ser Ala Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu
    45                  50                  55
```

Page 12

ccc	ttt	ttg	cca	aaa	gct	cca	gca	ttt	cag	cgg	gag	gat	gaa	cgg	gct	725
Pro	Phe	Leu	Pro	Lys	Ala	Pro	Ala	Phe	Gln	Arg	Glu	Asp	Glu	Arg	Ala
60				65					70					75

```
ccc ttt ttg cca aaa gct cca gca ttt cag cgg gag gat gaa cgg gct      725
Pro Phe Leu Pro Lys Ala Pro Ala Phe Gln Arg Glu Asp Glu Arg Ala
60              65                  70                  75

gac ttg tat ttt gat gcg ggt gat ctg ttg gtg ctg gcg aaa acg acc      773
Asp Leu Tyr Phe Asp Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr
                80                  85                  90

gtt cga aac tat gcg att gcg atc acg gaa acg gcg acg ccc gag ctc      821
Val Arg Asn Tyr Ala Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu
            95                  100                 105

agg aga gtg ctt gtt aaa caa atc aat gcg gcc att aag ttg cat gaa      869
Arg Arg Val Leu Val Lys Gln Ile Asn Ala Ala Ile Lys Leu His Glu
            110                 115                 120

caa gtt ttt tat ttt atg tac caa aga ggc tta tat ccc gcc tat aac      917
Gln Val Phe Tyr Phe Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn
        125             130                 135

ctc gtc gac ctg cta aaa ggc gac gcc atg cat gcg caa aaa gcg ata      965
Leu Val Asp Leu Leu Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile
140             145                 150                 155

tcg atg aga  taaaaaagcc agcgaggata gaatcctcac tggctctgtt           1014
Ser Met Arg
```

```
ttttgctatt ttacgattaa aaccggacac ttcactcttt tcgccacttt atggctgaca   1074

cttccgagca ccatttcctg caaagtgttc agccccctgc ttccgataat cacgatatca   1134

acatcatgat ggttggcgta cgatacaatg gccgggcccg gatccccgtg ctgcatcgtc   1194

atttgatagg gaacggccgc ctgtttaat ttattttcta tcgacagcag cctgctgcgc   1254

cgttcgcgtt cgagttctgt acggttttcg ctatgcagga cttcatgttt tgctctcgca   1314

taatccaata cataaatcat gtcgacgacc gcttcgtttg acatggaagc cagatgaatc   1374

gcatgatcgg cagctctttc agaatgcttg gaaccgtcag cagccagcag tatatgtcta   1434

tacacccttc atcacccgtt tcttagtgat ttgacactga acg                     1477
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<210> 10

<211> 158

<212> PRT

<213> Bacillus licheniformis

<400> 10

```
Met Thr Thr Lys Thr Leu Ala Trp His Glu Thr Leu Glu Leu His Glu
1               5                   10                  15


Leu Ile Ala Ala Gln Ser Val Gly Leu Val Lys Ile Lys Lys Ser Met
            20                  25                  30


Lys Lys Ile Ser Asp Pro Gln Leu Arg Gln Leu Tyr Ser Val Ser Ala
        35                  40                  45
```

```
Lys Ala Leu Glu Gln Asn Leu Arg Glu Leu Leu Pro Phe Leu Pro Lys
    50              55              60

Ala Pro Ala Phe Gln Arg Glu Asp Glu Arg Ala Asp Leu Tyr Phe Asp
65              70              75              80

Ala Gly Asp Leu Leu Val Leu Ala Lys Thr Thr Val Arg Asn Tyr Ala
                85              90              95

Ile Ala Ile Thr Glu Thr Ala Thr Pro Glu Leu Arg Arg Val Leu Val
            100             105             110

Lys Gln Ile Asn Ala Ala Ile Lys Leu His Glu Gln Val Phe Tyr Phe
        115             120             125

Met Tyr Gln Arg Gly Leu Tyr Pro Ala Tyr Asn Leu Val Asp Leu Leu
    130             135             140

Lys Gly Asp Ala Met His Ala Gln Lys Ala Ile Ser Met Arg
145             150             155
```

<210>   11

<211>   1752

<212>   DNA

<213>   Bacillus licheniformis

<220>

<221>   CDS

<222>   (183)..(1256)

<223>

<400>   11
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ctgacatgga cccactcatc ttgtaacctc ctgttcttcc tttttatgt  cctgatttat      60

acatacgcgc cgtaaagaca agtgtactga ggcaaatgac tgtttttgtt caaacttagg     120

cggtctgctt ccgggacagg ttttttttcac atatgatatg tcagctgaaa aaggaggaaa    180

tg atg atg agt gcc act gcc ttg ccg gcc ttt agg ctg cac att cat       227
   Met Met Ser Ala Thr Ala Leu Pro Ala Phe Arg Leu His Ile His
   1               5                   10                  15

ccg aag cat ctg ctt gag ttg aaa aaa gac gtc tgg agt gat gaa gcc       275
Pro Lys His Leu Leu Glu Leu Lys Lys Asp Val Trp Ser Asp Glu Ala
            20                  25                  30

gtt ccc ggc atg ctc ttg acc ggt tca gca aag acg cct gtc gca gtg       323
Val Pro Gly Met Leu Leu Thr Gly Ser Ala Lys Thr Pro Val Ala Val
            35                  40                  45
```

Page 14

```
tca tac aga ggg gcc cac acc cgc aaa ctg acg aaa aaa tcc tat ttc       371
Ser Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe
        50              55              60

att caa tat ccg gac aat aaa gaa aag gct gcg ttt cat ttg aac gcg       419
Ile Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala
65              70              75

gaa tat cat gat ccg tct ttc atc aga aac agg ctt tcc ttt cat ttt       467
Glu Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe
80              85              90              95

ttt gaa caa atc ggc gtc ctt gcg cca gca gca tca cac gtt ttc ctt       515
Phe Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu
                100             105             110

tat atc aat gaa aaa aaa gaa ggc atc tat tta aaa atc gaa tct gtt       563
Tyr Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val
                115             120             125

gac gat cat ttc tta aag agg aga aat tta gaa agg ggg gcc att tat       611
Asp Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr
        130             135             140

tat gcc gtt gat gac gat gct aat ttt tct ctg ctg agt tcc ttc aat       659
Tyr Ala Val Asp Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn
        145             150             155

aaa aag gct aag caa aat ctc atg cag gga tac gaa aga aaa acg ggt       707
Lys Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly
160             165             170             175

tca agc cgc cac gat gac tac ctc cat gag ttt atc tac ttt atc aat       755
Ser Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn
                180             185             190

acc gcc aaa gac gac ata ttt gaa aaa gaa atc aaa cgc tat ctc gat       803
Thr Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp
                195             200             205

gtc aaa caa tat ttg ctg tgg ctc atc ggc gcc gtc tgc acc caa aat       851
Val Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn
        210             215             220

ttc gac ggc ttt gtc cat aat tac gcg ctt tat tta aac ggt cgc aca       899
Phe Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr
225             230             235

aaa acg ttt caa atc att cca tgg gat tat gac gcg aca tgg gga cgg       947
Lys Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg
240             245             250             255

aat att cac ggg gaa gaa atg gag cac aac cgg att ccg gcg aaa ggc       995
Asn Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly
                260             265             270

tat aat acg ctg tct gca agg ctg ctc gac atc ccg gct ttt caa tcc      1043
Tyr Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser
        275             280             285

caa tac ttt aat tta atg aaa aat gtc ttg cac cgc caa ttt aca atc      1091
Gln Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile
        290             295             300

agc cgg ctt tcg cgg tat gcg gta aac tgg cac gag aca atc gcg cct      1139
Ser Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro
        305             310             315
```

```
ttt ctt gaa cat gat cct tat aca acc gtc aca tac agc cgg ctc gaa     1187
Phe Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu
320             325             330             335

gat gag caa aaa caa att ttt cat ttc atc gat cag agg aag cgg ttc     1235
Asp Glu Gln Lys Gln Ile Phe His Phe Ile Asp Gln Arg Lys Arg Phe
                340             345             350

ctg ctt ttc gag ctt tcc cga taatagactg tcgctgtcct ccgaaaaaaa       1286
Leu Leu Phe Glu Leu Ser Arg
            355
```

tgtcacattt tttgtcatat tggcgaaaaa aatccctttt acacaaaata aggtatacta	1346
gcaatatcaa ggacatcaat gcgctgaata cctgaaatta ccgactcaaa atacaaatcg	1406
aaagttggag actgccatga tgaacaataa aattgaagca aaaagactgg ccttatttga	1466
agctgccgaa aagttcggca tcaactccaa agaggccatt cgatgcagtc aggaattgga	1526
caacttgctg aatcaaagaa tgcaaaagga tgataactgc gtgcatgcgg aagaaagaaa	1586
aggccgccac acgtcatgac ctccgactgc aagctgcgcc tgatgccggc ctccttcctc	1646
ctccatttca tcatccgttg atttcgggtc gcagcttggg ctattcggcc attgtttttt	1706
gaacataaat catcgtgcaa ataccgtagg caagaatggc tgaagg	1752

<210> 12

<211> 358

<212> PRT

<213> Bacillus licheniformis

<400> 12

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Met Met Ser Ala Thr Ala Leu Pro Ala Phe Arg Leu His Ile His Pro
1               5               10              15

Lys His Leu Leu Glu Leu Lys Lys Asp Val Trp Ser Asp Glu Ala Val
            20              25              30

Pro Gly Met Leu Leu Thr Gly Ser Ala Lys Thr Pro Val Ala Val Ser
        35              40              45

Tyr Arg Gly Ala His Thr Arg Lys Leu Thr Lys Lys Ser Tyr Phe Ile
    50              55              60

Gln Tyr Pro Asp Asn Lys Glu Lys Ala Ala Phe His Leu Asn Ala Glu
65              70              75              80

Tyr His Asp Pro Ser Phe Ile Arg Asn Arg Leu Ser Phe His Phe Phe
                85              90              95

Glu Gln Ile Gly Val Leu Ala Pro Ala Ala Ser His Val Phe Leu Tyr
            100             105             110
```

Ile Asn Glu Lys Lys Glu Gly Ile Tyr Leu Lys Ile Glu Ser Val Asp
        115   120   125

Asp His Phe Leu Lys Arg Arg Asn Leu Glu Arg Gly Ala Ile Tyr Tyr
    130   135   140

Ala Val Asp Asp Asp Ala Asn Phe Ser Leu Leu Ser Ser Phe Asn Lys
145   150   155   160

Lys Ala Lys Gln Asn Leu Met Gln Gly Tyr Glu Arg Lys Thr Gly Ser
            165   170   175

Ser Arg His Asp Asp Tyr Leu His Glu Phe Ile Tyr Phe Ile Asn Thr
        180   185   190

Ala Lys Asp Asp Ile Phe Glu Lys Glu Ile Lys Arg Tyr Leu Asp Val
        195   200   205

Lys Gln Tyr Leu Leu Trp Leu Ile Gly Ala Val Cys Thr Gln Asn Phe
    210   215   220

Asp Gly Phe Val His Asn Tyr Ala Leu Tyr Leu Asn Gly Arg Thr Lys
225   230   235   240

Thr Phe Gln Ile Ile Pro Trp Asp Tyr Asp Ala Thr Trp Gly Arg Asn
            245   250   255

Ile His Gly Glu Glu Met Glu His Asn Arg Ile Pro Ala Lys Gly Tyr
        260   265   270

Asn Thr Leu Ser Ala Arg Leu Leu Asp Ile Pro Ala Phe Gln Ser Gln
        275   280   285

Tyr Phe Asn Leu Met Lys Asn Val Leu His Arg Gln Phe Thr Ile Ser
    290   295   300

Arg Leu Ser Arg Tyr Ala Val Asn Trp His Glu Thr Ile Ala Pro Phe
305   310   315   320

Leu Glu His Asp Pro Tyr Thr Thr Val Thr Tyr Ser Arg Leu Glu Asp
            325   330   335

Glu Gln Lys Gln Ile Phe His Phe Ile Asp Gln Arg Lys Arg Phe Leu
            340   345   350

Leu Phe Glu Leu Ser Arg
        355

<210> 13

<211>   1570

<212>   DNA

<213>   Bacillus licheniformis

<220>

<221>   CDS

<222>   (501)..(1067)

<223>

<400>   13

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accaaagtca aatcgtatcg cccgtttcac agcgcctttg atccgtgtcc gccgatcggc    60

aaaagatact acagaacccc tccaaatcta tatctaggtt ttcagccccg cggccttccg   120

cagttttccc cgatggaggc gctgcaaaaa gggacgcttt ggcccgtatt ttacgatcat   180

tatgaaaatc cgtatgaaga tgggaggtaa ggagggtgac gaactcttta ccgcaagact   240

attataaaag gcttcatgaa attcaggctg ttgattttgt catcgttgag ctgatgctat   300

accttgacac acatcccgat gataccgatg ccatcaaaca atacaaccag tatgccggat   360

tttccagaaa actgaaagcg aagtttgaat caaaatacgg ccctttgatt caaggaagcc   420

cggatcagac ggaatcctat tggagctgga aagaagtcc ttggccatgg caagtttaat   480

agaggaaggg agtcaggttc atg tgg ctt tat gag aaa aaa ctg cag tat cct   533
                       Met Trp Leu Tyr Glu Lys Lys Leu Gln Tyr Pro
                        1               5                  10

gtt agg gtg aga gaa tgc aat ccg aga ctt gcc aaa ttt ttg att gag    581
Val Arg Val Arg Glu Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu
             15                  20                  25

caa tac ggc gga gcg gac ggc gaa ttg gct gcg gcg ctt cgc tat ttg    629
Gln Tyr Gly Gly Ala Asp Gly Glu Leu Ala Ala Ala Leu Arg Tyr Leu
         30                  35                  40

aac cag cgc tac agc ata ccc gat aaa gtc gtc gga ctg ctg acg gac    677
Asn Gln Arg Tyr Ser Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp
     45                  50                  55

atc ggt acg gaa gag ttt gct cac ctt gaa atg att gcc acg atg gta    725
Ile Gly Thr Glu Glu Phe Ala His Leu Glu Met Ile Ala Thr Met Val
60                  65                  70                  75

tat aaa tta aca aaa gac gcg acg ccc gag cag atg aag gaa gcc ggg    773
Tyr Lys Leu Thr Lys Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly
                 80                  85                  90

ctc ggc gat cat tac gca gac cat gac aaa gcc ctg ttt tat cat aac    821
Leu Gly Asp His Tyr Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn
             95                 100                 105

gct gcc ggc gtt ccg ttc acc gct aca tac atc cag gca aaa ggc gat    869
Ala Ala Gly Val Pro Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp
         110                 115                 120

ccg att gcc gat tta tat gaa gat ata gcg gct gaa gaa aaa gcg agg    917
```

```
Pro Ile Ala Asp Leu Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg
    125             130             135

gct acg tat caa tgg ctg att gac atg tcg gat gat ccg gat tta aat      965
Ala Thr Tyr Gln Trp Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn
140             145             150             155

gac ggg ctg gcg ttt tta cgg gaa agg gaa atc gtt cat tca cag cgc     1013
Asp Gly Leu Ala Phe Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg
            160             165             170

ttc cgc gaa gct gtc gaa att ttg aag gaa gag cgc gac cgt aaa aaa     1061
Phe Arg Glu Ala Val Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys
        175             180             185

gtg ttt taaacagcaa aaagccgaaa atacgaccgt attttcggct ttttatttac     1117
Val Phe
```

```
tgcaccgggc tcgcaagcag ttctgctgcg cggtcgcgca gcacatattt ttgaactttt     1177
ccggatgcgg tcagcgggta ttcgtcgatc agaaatacgt actccggaat tttataatac     1237
gaaagctgtc ctttgcaaaa atctctgacg tcttcgagcg tcagcttttt gcccggcctg     1297
catttaataa aggcagccgt tttttccccg tactttcat ccggaacgcc gacaacctgt      1357
acatcgacaa tatcctcatg ttcataaagg aattcctcta tttcacgcgg gtaaatgttt     1417
tccccgccgc ggacgatcat atcttttaag cgcccggtaa tcctcacgta tccgtcccgg     1477
tccatttctg ccaaatctcc ggtatggagc cagccgtctt catcgatggc cttttttgtg     1537
gcttcatcca ttttatagta gcctttcatg acg                                  1570
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<210> 14

<211> 189

<212> PRT

<213> Bacillus licheniformis

<400> 14

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Met Trp Leu Tyr Glu Lys Lys Leu Gln Tyr Pro Val Arg Val Arg Glu
1               5               10              15

Cys Asn Pro Arg Leu Ala Lys Phe Leu Ile Glu Gln Tyr Gly Gly Ala
            20              25              30

Asp Gly Glu Leu Ala Ala Ala Leu Arg Tyr Leu Asn Gln Arg Tyr Ser
        35              40              45

Ile Pro Asp Lys Val Val Gly Leu Leu Thr Asp Ile Gly Thr Glu Glu
    50              55              60

Phe Ala His Leu Glu Met Ile Ala Thr Met Val Tyr Lys Leu Thr Lys
65              70              75              80
```

Page 19

Asp Ala Thr Pro Glu Gln Met Lys Glu Ala Gly Leu Gly Asp His Tyr
              85   90   95

Ala Asp His Asp Lys Ala Leu Phe Tyr His Asn Ala Ala Gly Val Pro
             100   105   110

Phe Thr Ala Thr Tyr Ile Gln Ala Lys Gly Asp Pro Ile Ala Asp Leu
         115   120   125

Tyr Glu Asp Ile Ala Ala Glu Glu Lys Ala Arg Ala Thr Tyr Gln Trp
    130   135   140

Leu Ile Asp Met Ser Asp Asp Pro Asp Leu Asn Asp Gly Leu Ala Phe
145   150   155   160

Leu Arg Glu Arg Glu Ile Val His Ser Gln Arg Phe Arg Glu Ala Val
             165   170   175

Glu Ile Leu Lys Glu Glu Arg Asp Arg Lys Lys Val Phe
             180   185

<210> 15

<211> 1241

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (519)..(1028)

<223>

<400> 15
agccttcctt tctttctaat attttttaaag aaattgaggt gagaaacaat tggcagattt   60
tgaaaaactt caagagaacg tagatccgat aatgaaatca gttgttaaaa atatcttgaa   120
aaatcgggga gtaaccagcg ataaagttcg gacgctctca gaagaagaaa aagaaaatat   180
tttcaatatg ctggaagatc taaaaaaaca aaccgatgct ttggttcaaa aacagaaaga   240
aaaagcagcc gcaccgaatg aaaaagggac aaagagagaa aagaacgctg atgcgtcatc   300
agaaatggc gagagaccaa gaagaagaag aaacagaaca aatagactga gagaaaaact   360
tcgacaacgg agggagcaag aaaacacagc aacagcggaa aattcaaccg agtcagatac   420
ttcagcagaa aaaaatgggg atttgtagta gggtatctgt cttatacaag ttaaggagtt   480
acaacattta ataatagtaa atggaaggag gaaaagaa atg gaa aca aga cca tat   536
                                           Met Glu Thr Arg Pro Tyr
                                           1   5

Page 20

```
tca tgg att gcg ctt gac ccg gaa tgc gaa cat cca ggc aac gat tat      584
Ser Trp Ile Ala Leu Asp Pro Glu Cys Glu His Pro Gly Asn Asp Tyr
            10              15              20

cac cct agt tat cct aag aaa aaa tta tgt gac gac tat act tgc aac      632
His Pro Ser Tyr Pro Lys Lys Lys Leu Cys Asp Asp Tyr Thr Cys Asn
        25              30              35

tgt ggt agg aaa ggg caa aat ggc ttt atc gat tct gac cta gat caa      680
Cys Gly Arg Lys Gly Gln Asn Gly Phe Ile Asp Ser Asp Leu Asp Gln
    40              45              50

ctt cat ctt aac aaa cag ctc tca gat gaa acg atc atc att aaa gac      728
Leu His Leu Asn Lys Gln Leu Ser Asp Glu Thr Ile Ile Ile Lys Asp
55              60              65              70

tct tgt gat gtt caa gtc tca act gaa gac aca caa acg ttg gca tca      776
Ser Cys Asp Val Gln Val Ser Thr Glu Asp Thr Gln Thr Leu Ala Ser
                75              80              85

gtc atg aca gct gca caa aca cta gct gtt act att att ctc gcc att      824
Val Met Thr Ala Ala Gln Thr Leu Ala Val Thr Ile Ile Leu Ala Ile
            90              95              100

atc gat gat cct gat cta gcc gaa ctt gtc aca act gat ctg ttg cag      872
Ile Asp Asp Pro Asp Leu Ala Glu Leu Val Thr Thr Asp Leu Leu Gln
        105             110             115

gta act gcc aat aaa caa acg aac aga caa aaa ttg gtg atc gat aat      920
Val Thr Ala Asn Lys Gln Thr Asn Arg Gln Lys Leu Val Ile Asp Asn
    120             125             130

tcc aga aat gta cat gtc aca acc gaa gat aca gac aca gct atc atc      968
Ser Arg Asn Val His Val Thr Thr Glu Asp Thr Asp Thr Ala Ile Ile
135             140             145             150

gta agc aca ttt gtt caa act gtt gta atc acc atc acc gcc ctt atc      1016
Val Ser Thr Phe Val Gln Thr Val Val Ile Thr Ile Thr Ala Leu Ile
            155             160             165

gtc ggc ctt cta taattcaaaa agcagagcca accagctctg cttttcttca         1068
Val Gly Leu Leu
            170

tttttataga cgattaccca caccaacaag ggcacgggta catatgttgt taaagactaa    1128

agtcaaatat ccctataaaa aggagctgaa atccatgagc tgcggaaaac accatggccg    1188

gcatgaaaat tgtgtatgcg atgcagtaga acagattata aaagaacagg atg          1241
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<210> 16

<211> 170

<212> PRT

<213> Bacillus licheniformis

<400> 16

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Met Glu Thr Arg Pro Tyr Ser Trp Ile Ala Leu Asp Pro Glu Cys Glu
1               5               10              15
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His Pro Gly Asn Asp Tyr His Pro Ser Tyr Pro Lys Lys Lys Leu Cys
            20                  25              30

Asp Asp Tyr Thr Cys Asn Cys Gly Arg Lys Gly Gln Asn Gly Phe Ile
            35              40              45

Asp Ser Asp Leu Asp Gln Leu His Leu Asn Lys Gln Leu Ser Asp Glu
    50                  55              60

Thr Ile Ile Ile Lys Asp Ser Cys Asp Val Gln Val Ser Thr Glu Asp
65              70              75              80

Thr Gln Thr Leu Ala Ser Val Met Thr Ala Ala Gln Thr Leu Ala Val
                85              90                  95

Thr Ile Ile Leu Ala Ile Ile Asp Asp Pro Asp Leu Ala Glu Leu Val
            100             105             110

Thr Thr Asp Leu Leu Gln Val Thr Ala Asn Lys Gln Thr Asn Arg Gln
        115             120             125

Lys Leu Val Ile Asp Asn Ser Arg Asn Val His Val Thr Thr Glu Asp
    130             135             140

Thr Asp Thr Ala Ile Ile Val Ser Thr Phe Val Gln Thr Val Val Ile
145             150             155             160

Thr Ile Thr Ala Leu Ile Val Gly Leu Leu
            165             170
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<210> 17

<211> 1516

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1013)

<223>

<400> 17
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ggccgggcca attcccggga ggttttccag gtgcggcgcc atatggacag atgccgcaaa     120
tgggagctcc gtacggtatg gggggatacg gacagcagcc tgcaggggga cagatgttta     180
acagaccgga agatgatgaa gactgattcg gaatgggacg atgatctatc gttccttttt     240
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tattgtggac cgctataaac attttcatgc tatttaacgg gaatgtctat aactgtcaag      300

ggtaactctt cgcatcccgc acatcctaaa aaagagcgca atgctcaaat tcagcggttt      360

tcacggggg  tactaccatt ggacagcaag ctgaaagtgt tttcggggat tttgcttttg      420

acagcaggtc tatctgcatg cggaacgaac gacgctatag ataatggaaa caatacgcgc      480

ccgatcggat attatctcaa atg atg cag atc gta atg cag ggt ctt gat aat      533
                      Met Met Gln Ile Val Met Gln Gly Leu Asp Asn
                       1               5                   10

gac ggc cct gtt aca gaa atg ctt gaa aac atg aac ggg aga cac ggt       581
Asp Gly Pro Val Thr Glu Met Leu Glu Asn Met Asn Gly Arg His Gly
              15                  20                  25

gca aca aac gta aac aat cga gcg gga aac ggc aat ccc gtt cca aca       629
Ala Thr Asn Val Asn Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr
          30                  35                  40

ggc gat gga act tac agc cgg gga gac atg aat tat cac aac cat ttg       677
Gly Asp Gly Thr Tyr Ser Arg Gly Asp Met Asn Tyr His Asn His Leu
      45                  50                  55

gtg aat acg gcg gat aca ggc tat gac aga ccg gaa aac cgt aaa atc       725
Val Asn Thr Ala Asp Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile
60                  65                  70                  75

tca agg aat atc act ggg cgc gtc aac aaa ttg aat tat gtt gac gaa       773
Ser Arg Asn Ile Thr Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu
                80                  85                  90

agc cag gca gtc gta acg aat gaa acg gtc atc atc gcc gta cgg tct       821
Ser Gln Ala Val Val Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser
            95                  100                 105

gat aaa agg ctg aca aat aac gag aga act caa att aga aaa gca gcc       869
Asp Lys Arg Leu Thr Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala
        110                 115                 120

aaa aca ttt gcc gga gac cgg acc gtt caa gtt gtc gag gac gac ggc       917
Lys Thr Phe Ala Gly Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly
        125                 130                 135

gca ttt aca agg ctg cgc gaa atg aac gat gat cct cag aac att agg       965
Ala Phe Thr Arg Leu Arg Glu Met Asn Asp Asp Pro Gln Asn Ile Arg
140                 145                 150                 155

gat cgc gga gac acg acg aat aac aat ttg aac cgc ttg cgg aac caa      1013
Asp Arg Gly Asp Thr Thr Asn Asn Asn Leu Asn Arg Leu Arg Asn Gln
                160                 165                 170

taacaagcag ggaattgccg gggattcccc ggcaattttt tataagcgct cggccgattc     1073

ctttacaaaa acggggaaaa ccgtataaag tgtacataga gacgagaatt attttggagg     1133

tagaaagtta tggctggcca ttctaaatgg aaaaatattc agagacgaaa aaatgcccaa     1193

gatgctaaac gcggcaaaat tttcatgaag cttgccaaag aaatatatgt agccgcgaaa     1253

gaaggggac cagatcccga atctaacgca agtctgcgtc tcgtcatcga taaagccaaa      1313

aatgcaaaca tgccaaatga caacatcgac cgcgccatca aaaagcttc cggcagccag      1373

gatggaaaaa gctatgagga aattacgtat gagggctacg gaccaagcgg tgtggctgtc     1433

atggtcaaat gtttgacaga taataaaaac cggacggcga caagcgtcag aaccgctttc     1493
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agcaaaaacg gcggcagctt ggg   1516

<210> 18

<211> 171

<212> PRT

<213> Bacillus licheniformis

<400> 18

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1   5   10   15

Glu Met Leu Glu Asn Met Asn Gly Arg His Gly Ala Thr Asn Val Asn
            20   25   30

Asn Arg Ala Gly Asn Gly Asn Pro Val Pro Thr Gly Asp Gly Thr Tyr
        35   40   45

Ser Arg Gly Asp Met Asn Tyr His Asn His Leu Val Asn Thr Ala Asp
    50   55   60

Thr Gly Tyr Asp Arg Pro Glu Asn Arg Lys Ile Ser Arg Asn Ile Thr
65   70   75   80

Gly Arg Val Asn Lys Leu Asn Tyr Val Asp Glu Ser Gln Ala Val Val
                85   90   95

Thr Asn Glu Thr Val Ile Ile Ala Val Arg Ser Asp Lys Arg Leu Thr
            100   105   110

Asn Asn Glu Arg Thr Gln Ile Arg Lys Ala Ala Lys Thr Phe Ala Gly
        115   120   125

Asp Arg Thr Val Gln Val Val Glu Asp Asp Gly Ala Phe Thr Arg Leu
    130   135   140

Arg Glu Met Asn Asp Asp Pro Gln Asn Ile Arg Asp Arg Gly Asp Thr
145   150   155   160

Thr Asn Asn Asn Leu Asn Arg Leu Arg Asn Gln
                165   170

<210> 19

<211> 1249

<212> DNA

<213> Bacillus licheniformis

Page 24

<220>

<221> CDS

<222> (501)..(746)

<223>

<400> 19

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atcaattgga accgttttt gcattttggg gaatatcggt ttttctatcg caaatggctg       120

gattgttttt atgctttcga tgtttgttct gacaatcggc gaaattttat gttttccttc       180

aatgaatgtc cttttggacg agctggctcc ggatcatatg aagggcgcgt attacggcat       240

gcaaaactta tacaacatcg gtgagttttt agggccttgg ctgggggaa tgatgcttgc        300

cttgtacggg ggaaaagccg tctttcttat tgctgcgtgt tcagtctttt tggctttagg       360

cgcttaccat gtgggaagga gaaagttttt atctgcacag cattatggtg tatcgccttt       420

ttcttattga aaatttaggc cgcttatgca tgaatcatta agaattaccc aacctaaaag       480

gtaaaaaagg agtatgaatc atg gac aca aca ttg ggc tac ctc cgt gag tca      533
                        Met Asp Thr Thr Leu Gly Tyr Leu Arg Glu Ser
                        1               5                   10

ctg tcg aat cac ctt gaa cac ggc ata gga caa aac att tac aga aaa        581
Leu Ser Asn His Leu Glu His Gly Ile Gly Gln Asn Ile Tyr Arg Lys
            15              20                  25

atc gtt tcc ggg cga tat gcc aat gag gaa gag ttt gtc gag cac ttg        629
Ile Val Ser Gly Arg Tyr Ala Asn Glu Glu Glu Phe Val Glu His Leu
        30                  35                  40

gag gag cgg gaa atg gaa ttt ctg aat caa gtg ctt gaa cat gag atg        677
Glu Glu Arg Glu Met Glu Phe Leu Asn Gln Val Leu Glu His Glu Met
    45                  50                  55

aaa tat gcg ctg aat gaa cag gac cat aaa cgg aca aga gaa tta aac        725
Lys Tyr Ala Leu Asn Glu Gln Asp His Lys Arg Thr Arg Glu Leu Asn
60                  65                  70                  75

gaa gtg tat gaa ctg ctg ttt tgaaaggcgg gaatgatcaa tgggtgcaat          776
Glu Val Tyr Glu Leu Leu Phe
                80

agagcggaac ggatacacgt ttgaaccgga atacagcgtg accagacaaa acggtgcgat       836

ccatgtatac cggcgcggcc ggtttgtcga ggagattccc tttgagtttc acggggagtt       896

tccagagcat gatttaattg aagagcttgt caatcattat tgttatgaaa ataaaatata       956

aggcttgaag aggctgccga ccgggcggct tttatttttg gatttttata tctataatcc      1016

gcttgcagtt ttttagaacg gcagcagaaa agctgccata aatatgacag ctcatgcatc      1076

gctatttttt cttttcgtcg tagtattgaa cagggtacat ggatccttcc gataccattt      1136

tgttatcttc gatatcatgc ggagacgggt gtcctgcttt ttcaaccggg aatgaatcta      1196

cgttgtgttt ttccgaaaag taagggatct tttctttgac gttttgcaag tac            1249
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<210> 20
<211> 82
<212> PRT
<213> Bacillus licheniformis

<400> 20

Met Asp Thr Thr Leu Gly Tyr Leu Arg Glu Ser Leu Ser Asn His Leu
1   5   10   15

Glu His Gly Ile Gly Gln Asn Ile Tyr Arg Lys Ile Val Ser Gly Arg
                20   25   30

Tyr Ala Asn Glu Glu Glu Phe Val Glu His Leu Glu Glu Arg Glu Met
            35   40   45

Glu Phe Leu Asn Gln Val Leu Glu His Glu Met Lys Tyr Ala Leu Asn
        50   55   60

Glu Gln Asp His Lys Arg Thr Arg Glu Leu Asn Glu Val Tyr Glu Leu
65   70   75   80

Leu Phe

<210> 21
<211> 1620
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (501)..(1121)
<223>

<400> 21
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atggctctca tgcagaagca cggggttaac ccgcttgccg gatgtttccc gatcttaatt   120
caaatgccga tttaatcgg attctatcat gccattatga gaacgcggga aatcgcagaa   180
cacagctttt tatggtttga ccttggggag cgtgatccgt atttcatttt gccgattctc   240
gccggtgtgt tcacattcat tcagcaaaag ctgatgatgg cgggaacagc gcagcaaaat   300

                              Page 26

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ccgcagatgg cgatgatgct ttggctgatg ccgatcatga tcgttgtatt tgcgatcagt    360

ttcccggcgg ctctttccct gtactgggta gtcggtaact tattcatgat tgctcaaacc    420

ttctttatca aagggcctga tctaaaggct gagagacagg aagcggcagc cggaggaaaa    480

aaatccggag gtaagaaaaa gtg aag gaa ctg act gct act gga cgt acc gtc    533
                       Val Lys Glu Leu Thr Ala Thr Gly Arg Thr Val
                        1               5                  10

gat gaa gca gtg caa tcc ggg ctt gaa cag ctg ggc ctt cat gca gat    581
Asp Glu Ala Val Gln Ser Gly Leu Glu Gln Leu Gly Leu His Ala Asp
            15              20              25

gat gtc gaa gtc gac gta gtt gat gaa gga aaa aag gga tta ttc ggc    629
Asp Val Glu Val Asp Val Val Asp Glu Gly Lys Lys Gly Leu Phe Gly
        30              35              40

att ttc ggt cat cgg tct gca gtc gtg aac att cgg gaa aaa ata gac    677
Ile Phe Gly His Arg Ser Ala Val Val Asn Ile Arg Glu Lys Ile Asp
    45              50              55

ccg gtt aaa gaa gca aaa caa tat ttg gaa aat gta att tcg aat atg    725
Pro Val Lys Glu Ala Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met
60              65              70              75

gga ata caa gcc cag gtg acg gca gaa gag gag tct aaa cga gtg gtt    773
Gly Ile Gln Ala Gln Val Thr Ala Glu Glu Glu Ser Lys Arg Val Val
            80              85              90

ttt cag ttg aaa gga gac aaa aca gct ctt tta att gga aaa agg gga    821
Phe Gln Leu Lys Gly Asp Lys Thr Ala Leu Leu Ile Gly Lys Arg Gly
            95              100             105

caa act tta aat gcc ctt gaa acg ctg acg cag ctc gtg ctc aat cgt    869
Gln Thr Leu Asn Ala Leu Glu Thr Leu Thr Gln Leu Val Leu Asn Arg
        110             115             120

cat tcc gac aga tat atc caa gcg gtg gtt gac gcc gaa gga tac cgc    917
His Ser Asp Arg Tyr Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg
        125             130             135

gca aag cgg aag gaa aca ctt gct cag ctg gca ttg aag ctt gct gac    965
Ala Lys Arg Lys Glu Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp
140             145             150             155

cag gcg gcc agg cag aaa aaa gac att cac ctg gag ccg atg cct tcc    1013
Gln Ala Ala Arg Gln Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser
            160             165             170

agt gag cgc aag gtc atc cat gat acg ctt gcg ggc tac tcg cag cat    1061
Ser Glu Arg Lys Val Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His
            175             180             185

atc gaa act tac tct acc ggt gaa gac cat aac cgg cac ctt gtc atc    1109
Ile Glu Thr Tyr Ser Thr Gly Glu Asp His Asn Arg His Leu Val Ile
            190             195             200

tca tat aaa aaa taacatgaaa accgaagttc ccaaaattgg ggcttcggtt    1161
Ser Tyr Lys Lys
205

tttttgccgt tgaaaatcga tgaaatgcag caaaatcagt ttaagttcta ttttttcagg    1221

cgtaagctgt tgatgaaaat gaaatttaat tgttattcac atgtggataa gttaaagtaa    1281

gtaatgatgg cttagaacgg ttgtggataa cggttcaagt cacttccact tcaattgaaa    1341
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ctatgttatc tttaaatttt gattacaata aaagtttttc atccgtatac gatgtttgga   1401

agatgacccg gcaaatgggg ataatagata taggaatgaa aaagagaggt gaaagccatg   1461

gataccatcg ctgcgatttc aacgccgatg ggagaagggg cgattgcgat cgtccggatg   1521

agcggccctg aggctcttgc gatcgccgat aaagtgtata aaggacctcg cggaaaaagg   1581

ctgagttccg tcgattcaca tacgattaac tacggtcat                          1620
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<210> 22

<211> 207

<212> PRT

<213> Bacillus licheniformis

<400> 22

Val Lys Glu Leu Thr Ala Thr Gly Arg Thr Val Asp Glu Ala Val Gln
1   5   10   15

Ser Gly Leu Glu Gln Leu Gly Leu His Ala Asp Asp Val Glu Val Asp
                20   25   30

Val Val Asp Glu Gly Lys Lys Gly Leu Phe Gly Ile Phe Gly His Arg
            35   40   45

Ser Ala Val Val Asn Ile Arg Glu Lys Ile Asp Pro Val Lys Glu Ala
        50   55   60

Lys Gln Tyr Leu Glu Asn Val Ile Ser Asn Met Gly Ile Gln Ala Gln
65   70   75   80

Val Thr Ala Glu Glu Glu Ser Lys Arg Val Val Phe Gln Leu Lys Gly
                85   90   95

Asp Lys Thr Ala Leu Leu Ile Gly Lys Arg Gly Gln Thr Leu Asn Ala
                100   105   110

Leu Glu Thr Leu Thr Gln Leu Val Leu Asn Arg His Ser Asp Arg Tyr
            115   120   125

Ile Gln Ala Val Val Asp Ala Glu Gly Tyr Arg Ala Lys Arg Lys Glu
        130   135   140

Thr Leu Ala Gln Leu Ala Leu Lys Leu Ala Asp Gln Ala Ala Arg Gln
145   150   155   160

Lys Lys Asp Ile His Leu Glu Pro Met Pro Ser Ser Glu Arg Lys Val
                165   170   175

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Ile His Asp Thr Leu Ala Gly Tyr Ser Gln His Ile Glu Thr Tyr Ser
            180                 185             190

Thr Gly Glu Asp His Asn Arg His Leu Val Ile Ser Tyr Lys Lys
        195             200                 205
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<210>   23

<211>   1614

<212>   DNA

<213>   Bacillus licheniformis

<220>

<221>   CDS

<222>   (501)..(1115)

<223>

<400>   23

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aatatagagg gaaagaaacg gcagaaccat tgtggagctt gcggccacga aaaaattcgc     180

aaaccacatg atcacaaggt ttttcttata aacagagatg cgaatcacct tcttaaaaaa     240

tttgaattcc ctttcattat aaatgaaatg cgaaagctgc atggaattga tgctctatag     300

aatgacgaaa aatgggcatt tgaaggaatt ttcaacattt tcagaaaata aaaccttaaa     360

tatagaaata taatgatata ataagagaaa tatgagcgta ctttggaaaa cattcagaag     420

actataggct tggataattt caatccgctg cgttaccacc ataagttttt tatattgaga     480

tagaaaggca ggtgtgaaag ttg gaa gcg agc acc tta ctg att att gat ttt     533
                      Leu Glu Ala Ser Thr Leu Leu Ile Ile Asp Phe
                       1               5                   10

gaa ttt aca atg cct gag gga aag tat cac ccg caa aat ttt ttc ccg       581
Glu Phe Thr Met Pro Glu Gly Lys Tyr His Pro Gln Asn Phe Phe Pro
             15                 20                  25

gaa atc ata gaa gca ggg att gta aag acg gtt cat gat gag gtg gtt       629
Glu Ile Ile Glu Ala Gly Ile Val Lys Thr Val His Asp Glu Val Val
         30                  35                  40

gag acg ttt tca agc tat att aag ccg aag aag ttc cct aaa tta acg       677
Glu Thr Phe Ser Ser Tyr Ile Lys Pro Lys Lys Phe Pro Lys Leu Thr
     45                  50                  55

agg cgc tgc aaa aat ttt ctc agc atc acg cag gaa cag gtt gac caa       725
Arg Arg Cys Lys Asn Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln
60                  65                  70                  75

ggc atc acg ttt aac gcg ctg att gaa aag ctg cgg gag ctt gat cct      773
Gly Ile Thr Phe Asn Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro
                 80                  85                  90
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Page 29

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gac cga aac agc gtc atc att aca tgg gga aac atg gat atg aaa gtg        821
Asp Arg Asn Ser Val Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val
            95                  100             105

ctg aag caa aat tgc atg ttc aac cat gtt ccg ttt ccg ttt aaa gga        869
Leu Lys Gln Asn Cys Met Phe Asn His Val Pro Phe Pro Phe Lys Gly
            110             115             120

gag atg agg gac ctt tcc atg gag tac aag gaa ttt ttc ggc gac aaa        917
Glu Met Arg Asp Leu Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys
    125             130             135

aca ttg acg aat ttg tgg aag gca gcg gaa gag tac ggc gat tca gga        965
Thr Leu Thr Asn Leu Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly
140             145             150             155

acg gga aaa cag cat aaa gcg ctt gac gac gcg atg aca acg tat aag       1013
Thr Gly Lys Gln His Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys
            160             165             170

ttg ttt cgg ctc gta gaa cgg gat aag aag tat ttg gaa aat ccg aag       1061
Leu Phe Arg Leu Val Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys
            175             180             185

ccg acg acg atc ggc gaa cgg gtt gac ctc tca aaa gtc ttt ccg cac       1109
Pro Thr Thr Ile Gly Glu Arg Val Asp Leu Ser Lys Val Phe Pro His
            190             195             200

gcc aca taaaaaccc aatctgacaa acagattggg ttatttgtgc aggaaatatt        1165
Ala Thr
205

cttttcaag cccatgaata agctcaagcg attttgccgc gtattcggac gaatcgtttt     1225

gcagatccgt ttttaagcgg ctcaaagctg agcggagcga atccgcataa tccggtacag     1285

cttcatcgaa cggcttcacc atgcggtgcg ggatattcgt ctgttcaccg taagcgagcg     1345

cttttcgttc atgaaaaaaa gggacgtctg cccgattggg atgatgaagg tcgccctgct     1405

tcggatgggt cagcacggcg aggattttga ccaggtagtg catcggttta acatccgtaa     1465

tttcgccgat gtagacgcct gttttataaa agcccttttac gcgatctccg acttgaaatt    1525

ggttgttcac tgcatctgcc tcctaatggt atcataataa ataaatggta aaaaaatcat     1585

ttcagggagg aagaaaaatg gcgccgttt                                       1614
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<210> 24

<211> 205

<212> PRT

<213> Bacillus licheniformis

<400> 24

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1               5               10              15

Glu Gly Lys Tyr His Pro Gln Asn Phe Phe Pro Glu Ile Ile Glu Ala
            20              25              30
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Gly Ile Val Lys Thr Val His Asp Glu Val Val Glu Thr Phe Ser Ser
        35   40   45

Tyr Ile Lys Pro Lys Lys Phe Pro Lys Leu Thr Arg Arg Cys Lys Asn
    50   55   60

Phe Leu Ser Ile Thr Gln Glu Gln Val Asp Gln Gly Ile Thr Phe Asn
65   70   75   80

Ala Leu Ile Glu Lys Leu Arg Glu Leu Asp Pro Asp Arg Asn Ser Val
                85   90   95

Ile Ile Thr Trp Gly Asn Met Asp Met Lys Val Leu Lys Gln Asn Cys
            100   105   110

Met Phe Asn His Val Pro Phe Pro Phe Lys Gly Glu Met Arg Asp Leu
        115   120   125

Ser Met Glu Tyr Lys Glu Phe Phe Gly Asp Lys Thr Leu Thr Asn Leu
    130   135   140

Trp Lys Ala Ala Glu Glu Tyr Gly Asp Ser Gly Thr Gly Lys Gln His
145   150   155   160

Lys Ala Leu Asp Asp Ala Met Thr Thr Tyr Lys Leu Phe Arg Leu Val
            165   170   175

Glu Arg Asp Lys Lys Tyr Leu Glu Asn Pro Lys Pro Thr Thr Ile Gly
            180   185   190

Glu Arg Val Asp Leu Ser Lys Val Phe Pro His Ala Thr
        195   200   205

<210>   25

<211>   1600

<212>   DNA

<213>   Bacillus licheniformis

<220>

<221>   CDS

<222>   (501)..(1097)

<223>

<400>   25
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tgttcatttt gaagtgtttt ggcaaagcct tcagcgaatt ttggatcttc aaagactttt      120

ttccaaaatt cagctccttt tttggaggtc attgtttttt caacggtttc tttgacagtt      180

ttttcatcca ttacaagtgt ttcatttaat ttgtcatcat ttaatatttc ttgaatcgct      240

ttttttccgt catctgtctt taatatatcg acaaccattt ttttggtttg atcatagtcc      300

atctcagctg cttggtccgt gggagcacaa gctgttacag atagaaacag aaaacagctt      360

atcgatagca ttgcggtctt gaacatgctt aagctccttt cgaaaactcg tcttaccttt      420

aatatgaatg tcttttaaaa atttatacat aacaaaatat cgctgttaca gcggtttatt      480

tagggggttgg gaagtctaca atg aaa agc cgt aat ctc gtc cga ttt ttc ttt      533
                          Met Lys Ser Arg Asn Leu Val Arg Phe Phe Phe
                           1               5                  10

tcc gta ttg ggt gtc gga gct ttg act aca agt att gtc ggt ttt gcc      581
Ser Val Leu Gly Val Gly Ala Leu Thr Thr Ser Ile Val Gly Phe Ala
            15              20              25

ata gag tgg gga aga tat aag gag ctg ttt ctt tcc ttc gag gta ttg      629
Ile Glu Trp Gly Arg Tyr Lys Glu Leu Phe Leu Ser Phe Glu Val Leu
        30              35              40

gag att ctg tct gtt ctt ttc tgg ttt atc ggg gtt ggc atg atc ttt      677
Glu Ile Leu Ser Val Leu Phe Trp Phe Ile Gly Val Gly Met Ile Phe
    45              50              55

agc gtg att gct caa atg gga ttt gtg att ttc tta acg att cac cgc      725
Ser Val Ile Ala Gln Met Gly Phe Val Ile Phe Leu Thr Ile His Arg
60              65              70              75

ttt gca ctg gaa att ttc aga tct cat tct ttg tgg aat tcg att cag      773
Phe Ala Leu Glu Ile Phe Arg Ser His Ser Leu Trp Asn Ser Ile Gln
                80              85              90

ctg ttt ttg att ata ttt gtc gcg ttt gac ttg gtt tac ttg cgc ttt      821
Leu Phe Leu Ile Ile Phe Val Ala Phe Asp Leu Val Tyr Leu Arg Phe
            95              100             105

ctg ttt ttt gaa aaa gat gga ggc tcc atc att ccg tac att tgg ctg      869
Leu Phe Phe Glu Lys Asp Gly Gly Ser Ile Ile Pro Tyr Ile Trp Leu
        110             115             120

ccg ctc ttt att ttg gcg gta ggc att gcg gcc gct tat gca aag caa      917
Pro Leu Phe Ile Leu Ala Val Gly Ile Ala Ala Ala Tyr Ala Lys Gln
    125             130             135

aaa cag tcc tct aaa aaa acg ttc gtt tcc gca tta ttt cta atg ttt      965
Lys Gln Ser Ser Lys Lys Thr Phe Val Ser Ala Leu Phe Leu Met Phe
140             145             150             155

gtt ttt act gtg atg gag tgg ttc ccg gcg tta agg gtc aat gaa gag     1013
Val Phe Thr Val Met Glu Trp Phe Pro Ala Leu Arg Val Asn Glu Glu
                160             165             170

gac tgg ctc tat tta atg ctg ctt cct tta tta gcc tgc aac gct ttt     1061
Asp Trp Leu Tyr Leu Met Leu Leu Pro Leu Leu Ala Cys Asn Ala Phe
            175             180             185

cag ctt tta atg ctg cca aaa ttt cag gca cgc gct tagaccggct          1107
Gln Leu Leu Met Leu Pro Lys Phe Gln Ala Arg Ala
            190             195

gctactttac ttctgaagat tttgcatccg tatttgcgat taattcgctg actgttacgt     1167
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ttttgagccc cttgcttctg agatggtgca cgatctctgg cagggcttct tttgtttgtt   1227

tggcggaatc tgaagcgtga aagagcacga tgtcaccggc gtttaccgtt ccatttacgt   1287

tttggacgat cttttgaacc cccgggttcg tccagtcatc cgagttaata ctataatgaa   1347

caacggtgta gccgtactgt ttagcaacat cgagtacgtc tttattaaac tggccggtcg   1407

gcggtcttaa aagcgtaagg tcgtcaagcc cgagtttttg aaaggagtgt cgtgcttttg   1467

ctaagtcttt tttgatctcg ctttttcttca tttgcgaata gtttttataa gcatagccca   1527

tactcccgat ctggtgacca tctttacgga ttctttctac gacatccggg tggcgctctg   1587

cccatgaagc tga                                                       1600
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<210> 26

<211> 199

<212> PRT

<213> Bacillus licheniformis

<400> 26

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Met Lys Ser Arg Asn Leu Val Arg Phe Phe Phe Ser Val Leu Gly Val
1               5                   10                  15

Gly Ala Leu Thr Thr Ser Ile Val Gly Phe Ala Ile Glu Trp Gly Arg
            20                  25                  30

Tyr Lys Glu Leu Phe Leu Ser Phe Glu Val Leu Glu Ile Leu Ser Val
        35                  40                  45

Leu Phe Trp Phe Ile Gly Val Gly Met Ile Phe Ser Val Ile Ala Gln
    50                  55                  60

Met Gly Phe Val Ile Phe Leu Thr Ile His Arg Phe Ala Leu Glu Ile
65                  70                  75                  80

Phe Arg Ser His Ser Leu Trp Asn Ser Ile Gln Leu Phe Leu Ile Ile
                85                  90                  95

Phe Val Ala Phe Asp Leu Val Tyr Leu Arg Phe Leu Phe Phe Glu Lys
                100                 105                 110

Asp Gly Gly Ser Ile Ile Pro Tyr Ile Trp Leu Pro Leu Phe Ile Leu
        115                 120                 125

Ala Val Gly Ile Ala Ala Ala Tyr Ala Lys Gln Lys Gln Ser Ser Lys
    130                 135                 140

Lys Thr Phe Val Ser Ala Leu Phe Leu Met Phe Val Phe Thr Val Met
145                 150                 155                 160
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Page 33

Glu Trp Phe Pro Ala Leu Arg Val Asn Glu Glu Asp Trp Leu Tyr Leu
165   170   175

Met Leu Leu Pro Leu Leu Ala Cys Asn Ala Phe Gln Leu Leu Met Leu
180   185   190

Pro Lys Phe Gln Ala Arg Ala
195

<210> 27

<211> 1991

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (489)..(1499)

<223>

<400> 27

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gatcagcgca cggtggaaat tccggtttgt tacggcggcc gtttcggccc tgatttggag     120

gaagtggccg acatcaacgg cctgactgca caggaagtca tcgatattca cacctcgggt     180

gagtacctcg tttatatgat cggctttgcg ccgggcttcc cttacctagg cggaatgtct     240

gaaaagatag ccgcaccgcg gcggtcatct cctcggactt cgattcccgc cggttcagtc     300

ggaatagccg gcatgcaaac aggcgtctat cccctttcaa cgccgggcgg ctggcagctg     360

atcggcaata cgccgcttga attattcaag ccttatgaac agcctccgag ccttctgaga     420

gcaggggata tcgtgaaatt tgtcagcgtg acagaagagg agtatcacgc gctgaaggag     480

gggaaatc ttg agc ata gaa gtg tta aag ccg ggt ctg atg aca acg gtt     530
         Leu Ser Ile Glu Val Leu Lys Pro Gly Leu Met Thr Thr Val
         1            5                  10

caa gac ttg ggc cgc aca ggt ttt caa aaa tac ggc gtg ctt gtc agc     578
Gln Asp Leu Gly Arg Thr Gly Phe Gln Lys Tyr Gly Val Leu Val Ser
15                  20              25                      30

ggt gcc atg gat gcc gat tct ttg cgg att gcc aat ctg ctc gcg ggg     626
Gly Ala Met Asp Ala Asp Ser Leu Arg Ile Ala Asn Leu Leu Ala Gly
                35              40                      45

aac agc cag aac gaa gct gcg ctt gaa gtg acg ctg atg ggg ccg ggg     674
Asn Ser Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly
            50                  55              60

ccg tct ctc cgc ttt caa aaa cct gct ctt ata gcg gtg acg ggc gct     722
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Pro Ser Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala
    65              70              75

gac ttt tca ctg atg gta aat gac gaa gaa gtc ccg ctt tgg cgc ccg        770
Asp Phe Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro
    80              85              90

gtt ttc atc aaa gag ggc agc gtg ttg aca ttc ggc atg tgc aag cgc        818
Val Phe Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg
95              100             105             110

gga agc cgt gca tat atg gca gtg gcc ggg gga att gat gtg ccg cct        866
Gly Ser Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro
                115             120             125

gta atg gaa agc aaa agc aca tat gtc aga gca gga ctc ggc ggc ttt        914
Val Met Glu Ser Lys Ser Thr Tyr Val Arg Ala Gly Leu Gly Gly Phe
            130             135             140

caa gga agg gcg ctt caa aag gga gac gtg tta tcg cta ggc agc ccg        962
Gln Gly Arg Ala Leu Gln Lys Gly Asp Val Leu Ser Leu Gly Ser Pro
        145             150             155

acg ccg ttg tcg gaa gcg ctg cac aga aag ctc gca gac gag ggc aaa        1010
Thr Pro Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys
    160             165             170

gaa cgg ggc ttt gcg gct ccg aag tgg gct gtc gac cgc aaa tat ttt        1058
Glu Arg Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe
175             180             185             190

ctc ccg cta aaa aag aac ccg gtc att cgt gtc atc aaa ggc gat cag        1106
Leu Pro Leu Lys Lys Asn Pro Val Ile Arg Val Ile Lys Gly Asp Gln
                195             200             205

ttt gct tgc ttt acc tca tca tca caa gag cgc ttt ttc gcg ggt cca        1154
Phe Ala Cys Phe Thr Ser Ser Ser Gln Glu Arg Phe Phe Ala Gly Pro
                210             215             220

ttc cgg gtg acg gct aaa tcc gac cgg atg ggg tac cgt ctt caa gga        1202
Phe Arg Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly
        225             230             235

gag gcg ctc gaa ctc act cag cct ctg gaa atg atc tct gaa gcg gta        1250
Glu Ala Leu Glu Leu Thr Gln Pro Leu Glu Met Ile Ser Glu Ala Val
    240             245             250

tca ttc gga acg att caa gtg ccg ccc gac ggc aat ccg atc gtt ctt        1298
Ser Phe Gly Thr Ile Gln Val Pro Pro Asp Gly Asn Pro Ile Val Leu
255             260             265             270

ctc gca gac agg cag aca gcg ggc gga tac ccg aga atc gcc cat atc        1346
Leu Ala Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile
                275             280             285

gca tca gct gat ttt tct cag gtc acg cag atg atg ccg ggc gag cag        1394
Ala Ser Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln
                290             295             300

gtg cag ttt cag ctt gtc agc ctt cag gaa gca gag cgc gtt tac atc        1442
Val Gln Phe Gln Leu Val Ser Leu Gln Glu Ala Glu Arg Val Tyr Ile
        305             310             315

gaa cgg gag acg aaa atc agc gaa ctt tct gcc cga ttg aag ctt gaa        1490
Glu Arg Glu Thr Lys Ile Ser Glu Leu Ser Ala Arg Leu Lys Leu Glu
320             325             330

tac atg tta tgataggtgt gatgtgtatc aggaggggga aggcatggaa             1539
Tyr Met Leu
```

Tyr Met Leu
335

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cataaaaaca aaacagtcgt caaagccatg accctgctca atctgttcct gacgagagaa    1599

aggctctcgc tgggcgacat gattgagctg acaggcatgc cgaaaacatc tgtctaccgc    1659

atggtttgtt ctctcgaaga aatgggtttt ctcgaccgcg acgagaacgg gatgtatagc    1719

ttaggactgc tgtttttgca atacggccac cttgtttcag aaaggcttga tattcgaaaa    1779

atcgctctgc ccatcatgga agaactccgc gatgacgtgg atgaagccgt ccatttaatt    1839

gtaaggcagg gaaatgaagc aatgtatata gaaaaaattg agggcacgca gaccgttcgc    1899

ctctatacag cgatcgggag gcggtcccct ttatatgccg gagcctgtgc gagaagcatt    1959

ctgacgtttt tgcctgaaga ggagcgggat gc                                 1991
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<210> 28

<211> 337

<212> PRT

<213> Bacillus licheniformis

<400> 28

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1               5               10                  15


Leu Gly Arg Thr Gly Phe Gln Lys Tyr Gly Val Leu Val Ser Gly Ala
            20              25                  30


Met Asp Ala Asp Ser Leu Arg Ile Ala Asn Leu Leu Ala Gly Asn Ser
        35                  40                  45


Gln Asn Glu Ala Ala Leu Glu Val Thr Leu Met Gly Pro Gly Pro Ser
    50                  55                  60


Leu Arg Phe Gln Lys Pro Ala Leu Ile Ala Val Thr Gly Ala Asp Phe
65                  70                  75                  80


Ser Leu Met Val Asn Asp Glu Glu Val Pro Leu Trp Arg Pro Val Phe
                85                  90                  95


Ile Lys Glu Gly Ser Val Leu Thr Phe Gly Met Cys Lys Arg Gly Ser
                100                 105                 110


Arg Ala Tyr Met Ala Val Ala Gly Gly Ile Asp Val Pro Pro Val Met
        115                 120                 125


Glu Ser Lys Ser Thr Tyr Val Arg Ala Gly Leu Gly Gly Phe Gln Gly
    130                 135                 140
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Arg Ala Leu Gln Lys Gly Asp Val Leu Ser Leu Gly Ser Pro Thr Pro
145   150   155   160

Leu Ser Glu Ala Leu His Arg Lys Leu Ala Asp Glu Gly Lys Glu Arg
                165   170   175

Gly Phe Ala Ala Pro Lys Trp Ala Val Asp Arg Lys Tyr Phe Leu Pro
                180   185   190

Leu Lys Lys Asn Pro Val Ile Arg Val Ile Lys Gly Asp Gln Phe Ala
                195   200   205

Cys Phe Thr Ser Ser Ser Gln Glu Arg Phe Phe Ala Gly Pro Phe Arg
210   215   220

Val Thr Ala Lys Ser Asp Arg Met Gly Tyr Arg Leu Gln Gly Glu Ala
225   230   235   240

Leu Glu Leu Thr Gln Pro Leu Glu Met Ile Ser Glu Ala Val Ser Phe
                245   250   255

Gly Thr Ile Gln Val Pro Pro Asp Gly Asn Pro Ile Val Leu Leu Ala
                260   265   270

Asp Arg Gln Thr Ala Gly Gly Tyr Pro Arg Ile Ala His Ile Ala Ser
                275   280   285

Ala Asp Phe Ser Gln Val Thr Gln Met Met Pro Gly Glu Gln Val Gln
290   295   300

Phe Gln Leu Val Ser Leu Gln Glu Ala Glu Arg Val Tyr Ile Glu Arg
305   310   315   320

Glu Thr Lys Ile Ser Glu Leu Ser Ala Arg Leu Lys Leu Glu Tyr Met
                325   330   335

Leu

<210>   29

<211>   2287

<212>   DNA

<213>   Bacillus licheniformis

<220>

<221>   CDS

<222>   (501)..(1784)

Page 37

<223>

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tatgagctgc ttacatttaa ctggatggcc cattcgctga cgcttgaata tgaggtgatc     180

ggtcaagtca aggatttgtc agcttatgaa gaaaggctcg tcgttctcat cagaaagctg     240

tttgggattt ttgacgatgc cgttttgaaa ggcagcgaca atcatctgac gatcacgctg     300

cagacggacg gtccggacga ccgcctcgtc atctttctcg atttccacgg cgtattcaca     360

aagctgaccg gtatcaaaga ctttcatcat tcactggccg acttttatga aatcaagcgg     420

tttgatgtaa cagaccgtga gtgcatcgcc gaaattcata tcaagtaaag cggttttttta    480
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ggaatagaac ggaggacatt atg ttt gtt gat cag gtg aaa ata tac gta aaa      533
                        Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys
                        1               5                   10

ggc gga gac gga ggc aac ggt atg gtt gct ttc cgc cgc gaa aaa tat        581
Gly Gly Asp Gly Gly Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr
            15              20              25

gtg cca aaa gga ggc cct gcc gga ggt gac ggc gga aaa ggc gga gac        629
Val Pro Lys Gly Gly Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp
        30                  35                  40

gtc gtt ttc aaa gtt gac gaa ggt ctc agc acg ctg atg gat ttt aga        677
Val Val Phe Lys Val Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg
    45                  50                  55

tat caa aga cat ttt aag gca gcg cgc gga gaa cac ggc atg tct aaa        725
Tyr Gln Arg His Phe Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys
60                  65                  70                  75

aac cag cac ggc cga aat gcc gaa gac atg gtt gtg aaa gtc ccg ccc        773
Asn Gln His Gly Arg Asn Ala Glu Asp Met Val Val Lys Val Pro Pro
                    80                  85                  90

ggc acg gtt gtc att gac gat gat aca aaa cag gtc atc gct gat tta        821
Gly Thr Val Val Ile Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu
                95                  100                 105

acg gag cac gga cag gaa gcc gtc atc gca aaa ggg gga cgc ggc gga        869
Thr Glu His Gly Gln Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly
        110                 115                 120

cgg ggc aat aca cgt ttt gcg acg cct gcc aac ccg gcg ccg cag ctt        917
Arg Gly Asn Thr Arg Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu
    125                 130                 135

tct gaa aac ggc gaa ccc ggc aag gag cgc tat att gtt ctc gag ctg        965
Ser Glu Asn Gly Glu Pro Gly Lys Glu Arg Tyr Ile Val Leu Glu Leu
140                 145                 150                 155

aaa gtt ttg gca gat gtc ggt ctt gtc ggc ttc cca agc gtc gga aaa       1013
Lys Val Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys
                160                 165                 170

tca acg ctc ctg tct gtc gtg tct tcg gcc aag ccg aaa att gcc gat       1061
Ser Thr Leu Leu Ser Val Val Ser Ser Ala Lys Pro Lys Ile Ala Asp
            175                 180                 185
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tac cac ttt aca acg ctg aac ccg aat ctc gga atg gtc gaa acg gaa    1109
Tyr His Phe Thr Thr Leu Asn Pro Asn Leu Gly Met Val Glu Thr Glu
        190             195                 200

gac ggc cgc agc ttt gta atg gcg gat ctt ccg gga ctg att gag ggg    1157
Asp Gly Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly
    205             210             215

gcg cac gaa gga gtt ggc ctc gga cac caa ttc ctc agg cat atc gaa    1205
Ala His Glu Gly Val Gly Leu Gly His Gln Phe Leu Arg His Ile Glu
220             225             230                 235

aga acg cgc gtc atc gtg cac gtt att gac atg tcg ggt ctt gaa ggg    1253
Arg Thr Arg Val Ile Val His Val Ile Asp Met Ser Gly Leu Glu Gly
            240             245             250

cgc gac ccg tat gaa gat tat gtg acc att aat aaa gag ctt gaa cag    1301
Arg Asp Pro Tyr Glu Asp Tyr Val Thr Ile Asn Lys Glu Leu Glu Gln
        255             260             265

tat aat ctc agg ctg aca gaa cgt cct caa att att gtc gcc aat aaa    1349
Tyr Asn Leu Arg Leu Thr Glu Arg Pro Gln Ile Ile Val Ala Asn Lys
        270             275             280

atg gat atg ccg gat gcg gaa gaa aat ctg aag gct ttc aaa gaa aag    1397
Met Asp Met Pro Asp Ala Glu Glu Asn Leu Lys Ala Phe Lys Glu Lys
    285             290             295

ctc aca gat gat tat cct gtt ttt cca atc agc gcg gtg acc aga caa    1445
Leu Thr Asp Asp Tyr Pro Val Phe Pro Ile Ser Ala Val Thr Arg Gln
300             305             310             315

ggc ttg agg gat ctg ctg ttt gaa att gcc gac cgt ttg gaa acg acg    1493
Gly Leu Arg Asp Leu Leu Phe Glu Ile Ala Asp Arg Leu Glu Thr Thr
        320             325             330

ccg gaa ttc ccg ctc tac gac gaa gaa gac atg gct gaa aac aga gtc    1541
Pro Glu Phe Pro Leu Tyr Asp Glu Glu Asp Met Ala Glu Asn Arg Val
        335             340             345

atg tat aag ctt gag gat gag gaa gcg ccg ttt gag atc agc cgt gat    1589
Met Tyr Lys Leu Glu Asp Glu Glu Ala Pro Phe Glu Ile Ser Arg Asp
        350             355             360

cct gac ggc acc ttc gtg ctc agc gga gcc aag ctt gaa cgc tta ttt    1637
Pro Asp Gly Thr Phe Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe
365             370             375

aaa atg acg gac ttt tca aga gat gag tct gtt aag cgt ttt gcc aga    1685
Lys Met Thr Asp Phe Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg
380             385             390             395

cag ctt cgc gga atg ggc gtc gat gat gcg ctt cgg gcc cgc ggt gca    1733
Gln Leu Arg Gly Met Gly Val Asp Asp Ala Leu Arg Ala Arg Gly Ala
                400             405             410

aaa gac ggg gat acg atc cgt ctt ctc gaa ttt gaa ttt gaa ttt atc    1781
Lys Asp Gly Asp Thr Ile Arg Leu Leu Glu Phe Glu Phe Glu Phe Ile
            415             420             425

gac tgatcatacc ggagagtttg ccaagcaagc tctccgactt ttagctgaaa        1834
Asp


ggaacgccct tcctttcgca ggatcaatgt aaaggaatca gggtttttaa aaggagagaa  1894

aagtctgtga aagaggagac cttttatctt gtcagggaag acgtgctgcc ggaggcaatg  1954
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cggaaaacac ttgaggtcaa aaagctgatt gagcggaaaa aagcggaatc tgtagctgaa    2014

gccgtacaaa aggtagattt gagccgaagc gctttttata agtacagaga tgcggttttt    2074

ccttttttata cgatggtcaa ggaacagatt atcacgcttt tttttcattt ggaggaccgc    2134

tcaggaacgc tgtcccatct gctgcaagtg gtagctgaat cgggctgcaa tgtgctgtcg    2194

atccaccaga ccatccctct tcaaggaaga gcgaatgtca cgctctctgt cagtacgaga    2254

ggcatggatg aaaatatcga tttgctgatg aac                                 2287
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<210> 30

<211> 428

<212> PRT

<213> Bacillus licheniformis

<400> 30

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Met Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly
1               5                  10                  15


Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly
            20                  25                  30


Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val
        35                  40                  45


Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe
    50                  55                  60


Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg
65                  70                  75                  80


Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile
                85                  90                  95


Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln
            100                 105                 110


Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg
            115                 120                 125


Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu
        130                 135                 140


Pro Gly Lys Glu Arg Tyr Ile Val Leu Glu Leu Lys Val Leu Ala Asp
145                 150                 155                 160


Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Ser
                165                 170                 175
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Page 40

Val Val Ser Ser Ala Lys Pro Lys Ile Ala Asp Tyr His Phe Thr Thr
                180   185   190

Leu Asn Pro Asn Leu Gly Met Val Glu Thr Glu Asp Gly Arg Ser Phe
        195   200   205

Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala His Glu Gly Val
    210   215   220

Gly Leu Gly His Gln Phe Leu Arg His Ile Glu Arg Thr Arg Val Ile
225   230   235   240

Val His Val Ile Asp Met Ser Gly Leu Glu Gly Arg Asp Pro Tyr Glu
            245   250   255

Asp Tyr Val Thr Ile Asn Lys Glu Leu Glu Gln Tyr Asn Leu Arg Leu
            260   265   270

Thr Glu Arg Pro Gln Ile Ile Val Ala Asn Lys Met Asp Met Pro Asp
        275   280   285

Ala Glu Glu Asn Leu Lys Ala Phe Lys Glu Lys Leu Thr Asp Asp Tyr
    290   295   300

Pro Val Phe Pro Ile Ser Ala Val Thr Arg Gln Gly Leu Arg Asp Leu
305   310   315   320

Leu Phe Glu Ile Ala Asp Arg Leu Glu Thr Thr Pro Glu Phe Pro Leu
            325   330   335

Tyr Asp Glu Glu Asp Met Ala Glu Asn Arg Val Met Tyr Lys Leu Glu
            340   345   350

Asp Glu Glu Ala Pro Phe Glu Ile Ser Arg Asp Pro Asp Gly Thr Phe
        355   360   365

Val Leu Ser Gly Ala Lys Leu Glu Arg Leu Phe Lys Met Thr Asp Phe
    370   375   380

Ser Arg Asp Glu Ser Val Lys Arg Phe Ala Arg Gln Leu Arg Gly Met
385   390   395   400

Gly Val Asp Asp Ala Leu Arg Ala Arg Gly Ala Lys Asp Gly Asp Thr
            405   410   415

Ile Arg Leu Leu Glu Phe Glu Phe Glu Phe Ile Asp
            420   425

<210> 31

<211> 2115

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1616)

<223>

<400> 31

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gttccagcgt ttgatctatt gcattgtgca gcgcctgaac atcaagagtc ttcatggcat   180

tctcctctaa tccttttcat tacaatcagt atatagttta ccactttata gaaagtactt   240

ggtgaatata tcctgttcaa ccatgaaaat gaatcattgg gcttaggtca ttatttctat   300

tgattcattt cgattaccgt aaacaagttt gttgtagcat tctttaggct ctgtgactaa   360

accaaaaagc catttgtttt aaattggtct ttcggtatca cgaaaatttc gttttttggg   420

ctgatagaag ttttgcaatt atgaattgta tgttaatctt taacataaaa aggatgttag   480
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ctggaaggga atgatggcag ttg gag act atc ccg tct tca gaa gtt gga atc   533
                          Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile
                          1               5                      10
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aaa ata aac cgc tgg tac aac gaa att caa aaa tta aac gta ata gaa   581
Lys Ile Asn Arg Trp Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu
            15                  20                  25
```

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gca gaa cga tta aag gcg gaa gtt cac tta gct ata gaa aga atg gaa   629
Ala Glu Arg Leu Lys Ala Glu Val His Leu Ala Ile Glu Arg Met Glu
        30                  35                  40
```

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gaa gat cag gac ttg ctt tcc tat tat cag ctt atg aat ttt aga cat   677
Glu Asp Gln Asp Leu Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His
    45                  50                  55
```

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gag tta atg ttg gaa tat ctt ttc ccg gca gaa aaa aag ctg agc aaa   725
Glu Leu Met Leu Glu Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys
60                  65                  70                  75
```

```
tct gat tat ctt agg gaa att gag gga cag gga aga aaa ttg tca ggc   773
Ser Asp Tyr Leu Arg Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly
                80                  85                  90
```

```
ttg ctc gaa tac tat ttt tcc ttt ttc acc gga atg tat cat ttt tct   821
Leu Leu Glu Tyr Tyr Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser
                95                  100                 105
```

```
cgc gga aaa tac ata aag gca atc aag gca tat aga gca gca gaa aaa   869
Arg Gly Lys Tyr Ile Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys
        110                 115                 120
```

```
aag ttg acg aaa gtt tca gat aaa ata gaa aag gct gaa ttc tat tat   917
```

Lys Leu Thr Lys Val Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr
125   130   135

aag atg gcg gaa gtg ttt tat cat atg aaa cag act cat atg tca atg   965
Lys Met Ala Glu Val Phe Tyr His Met Lys Gln Thr His Met Ser Met
140   145   150   155

tat tat gtg tct ctc gct tat gat att tat aaa tcc tat gat gca tat   1013
Tyr Tyr Val Ser Leu Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr
160   165   170

gtg att cga aga att aat tgt cta ttc gtt gtt gct ggg aat tac att   1061
Val Ile Arg Arg Ile Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile
175   180   185

gat tta tca acc cat gat caa gct tta ccg cat ctt tta agc gct aag   1109
Asp Leu Ser Thr His Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys
190   195   200

gaa tcc gcg gaa gac att caa aac aag gcg atc gtt gca aag gct ctt   1157
Glu Ser Ala Glu Asp Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu
205   210   215

tta aat gta gca tat tgt tat aat gca atg gag aga cca aca aaa gct   1205
Leu Asn Val Ala Tyr Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala
220   225   230   235

att gaa tac ttt cat aag gcg att gat gta gca aag gaa ata aag gca   1253
Ile Glu Tyr Phe His Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala
240   245   250

aaa gaa ctg act cag gct tat tat gat ttg gca tta att cac ttt cga   1301
Lys Glu Leu Thr Gln Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg
255   260   265

aat aac gaa aat att gaa gga cga aaa ttt tat gaa aag gcg ctt gaa   1349
Asn Asn Glu Asn Ile Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu
270   275   280

agt gcg cgg gta ttt gaa gat gaa tta ttc ctg tgt ctg ttg gat gtt   1397
Ser Ala Arg Val Phe Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val
285   290   295

tta gag gca ctg ttt ata aaa tca gct aat aag tca gag gta cta gaa   1445
Leu Glu Ala Leu Phe Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu
300   305   310   315

aca atg aaa cca tta cgg gat agt cgt ggt tac ccc tat ctt gag gaa   1493
Thr Met Lys Pro Leu Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu
320   325   330

ctg gca tta gaa gca gct cta ttc tat act agg aat gag cgg cca aat   1541
Leu Ala Leu Glu Ala Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn
335   340   345

gat tcc ata ttt ttt tat gat cag atg gtg cag gct cag aaa caa atc   1589
Asp Ser Ile Phe Phe Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile
350   355   360

aaa agg ggc gac ttt ctg tat gaa atc taagctgttt ctttcgctga   1636
Lys Arg Gly Asp Phe Leu Tyr Glu Ile
365   370

cccttgcttt gggcttgttg gtcgtgtcga gcgcttccat tcacacatct gttgaacaac 1696

aacatgcaga attttctgta gcatctaggc tcgcaacata attgtgtttg ggcaggtcat 1756

gtgatggcct gcctttttgg tgaaagaatt attttagttt gaaaaccaga acgattgtgt 1816

```
taatactcat ctttcttcgt cccttgtgtt ggaattttca tcatatcaat atttgaatat   1876

gcggctgtcc gcattattaa caattttaaa tttttttgcac aaattttata caaaggcaga   1936

caaaaacctt gatatatcaa tggttctatg ggtatattca accacgacca ccgatatcgc   1996

taaaaaccgt attgccaaac gacgaaagag cgttccttac acaaggaatg ctctttttgt   2056

ttattcctca tcaaagcgga gagccgccaa cataaacgca atgaccaact gttgtccgc    2115
```

<210> 32

<211> 372

<212> PRT

<213> Bacillus licheniformis

<400> 32

Leu Glu Thr Ile Pro Ser Ser Glu Val Gly Ile Lys Ile Asn Arg Trp
1   5   10   15

Tyr Asn Glu Ile Gln Lys Leu Asn Val Ile Glu Ala Glu Arg Leu Lys
            20   25   30

Ala Glu Val His Leu Ala Ile Glu Arg Met Glu Glu Asp Gln Asp Leu
        35   40   45

Leu Ser Tyr Tyr Gln Leu Met Asn Phe Arg His Glu Leu Met Leu Glu
    50   55   60

Tyr Leu Phe Pro Ala Glu Lys Lys Leu Ser Lys Ser Asp Tyr Leu Arg
65   70   75   80

Glu Ile Glu Gly Gln Gly Arg Lys Leu Ser Gly Leu Leu Glu Tyr Tyr
                85   90   95

Phe Ser Phe Phe Thr Gly Met Tyr His Phe Ser Arg Gly Lys Tyr Ile
            100   105   110

Lys Ala Ile Lys Ala Tyr Arg Ala Ala Glu Lys Lys Leu Thr Lys Val
        115   120   125

Ser Asp Lys Ile Glu Lys Ala Glu Phe Tyr Tyr Lys Met Ala Glu Val
    130   135   140

Phe Tyr His Met Lys Gln Thr His Met Ser Met Tyr Tyr Val Ser Leu
145   150   155   160

Ala Tyr Asp Ile Tyr Lys Ser Tyr Asp Ala Tyr Val Ile Arg Arg Ile
                165   170   175

Page 44
```

```
Asn Cys Leu Phe Val Val Ala Gly Asn Tyr Ile Asp Leu Ser Thr His
            180                 185             190

Asp Gln Ala Leu Pro His Leu Leu Ser Ala Lys Glu Ser Ala Glu Asp
            195                 200             205

Ile Gln Asn Lys Ala Ile Val Ala Lys Ala Leu Leu Asn Val Ala Tyr
    210             215             220

Cys Tyr Asn Ala Met Glu Arg Pro Thr Lys Ala Ile Glu Tyr Phe His
225             230             235             240

Lys Ala Ile Asp Val Ala Lys Glu Ile Lys Ala Lys Glu Leu Thr Gln
                245             250             255

Ala Tyr Tyr Asp Leu Ala Leu Ile His Phe Arg Asn Asn Glu Asn Ile
            260             265             270

Glu Gly Arg Lys Phe Tyr Glu Lys Ala Leu Glu Ser Ala Arg Val Phe
            275             280             285

Glu Asp Glu Leu Phe Leu Cys Leu Leu Asp Val Leu Glu Ala Leu Phe
    290             295             300

Ile Lys Ser Ala Asn Lys Ser Glu Val Leu Glu Thr Met Lys Pro Leu
305             310             315             320

Arg Asp Ser Arg Gly Tyr Pro Tyr Leu Glu Glu Leu Ala Leu Glu Ala
            325             330             335

Ala Leu Phe Tyr Thr Arg Asn Glu Arg Pro Asn Asp Ser Ile Phe Phe
            340             345             350

Tyr Asp Gln Met Val Gln Ala Gln Lys Gln Ile Lys Arg Gly Asp Phe
            355             360             365

Leu Tyr Glu Ile
    370
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<210> 33

<211> 2077

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1574)

Page 45

<223>

<400> 33

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ttgattaaag tggaaatatt ttaaaaaaca tgtatggtaa ttaaaaatct tttcgtcaat      60

aaatattatg gtcttttttcc tactttaaca aggcataatc tttccctcta ttgaatgtaa     120

tatagtaaag cgaatagagg agggtataca aatgaatcct tactatatga tgctcttatg     180

ttatgtccta tcgatcatcc actttttaat aggctaccgg gaagccctga aaataagcgg     240

ggttgacggg ctggtcaacg gaaccgcaat gatctcctgt attccgcttg gcgcggtttt     300

cgcttttttc gcgcactttt tttggaaaat gacgatttaa tttcgggaat gaattttttc     360

gccaacaaac atgcatttcc gtgttattca cagacggcgg cagtttatgc tatgattaat     420

agaacttcaa tttacaaaaa attcacaaag attggaggga aaagaatggc caaagccggg     480

cttctcaaga agtcgccaat atg ctg aac gac tgg tac ata ctg atg aaa aaa     533
                       Met Leu Asn Asp Trp Tyr Ile Leu Met Lys Lys
                        1               5                  10
```

```
cga gac att tca ggt tca atc gaa atg aaa gat gac ata gat aaa gca      581
Arg Asp Ile Ser Gly Ser Ile Glu Met Lys Asp Asp Ile Asp Lys Ala
             15                  20                  25
```

```
att gaa aag atg gaa gaa gat cat gac gtt ctt ctc tat tat caa atg      629
Ile Glu Lys Met Glu Glu Asp His Asp Val Leu Leu Tyr Tyr Gln Met
         30                  35                  40
```

```
ctg gat ttt cgc tta agg ctt ctt ctt gaa gat atc tcc caa tct tcc      677
Leu Asp Phe Arg Leu Arg Leu Leu Leu Glu Asp Ile Ser Gln Ser Ser
     45                  50                  55
```

```
aca gaa aaa ttg gaa gcc atc agt ttt aag gac aaa gat cca aaa agt      725
Thr Glu Lys Leu Glu Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser
60                  65                  70                  75
```

```
acg gac gat aag ctg aat tat tat ttt tat ctg ttc aaa ggg att tat      773
Thr Asp Asp Lys Leu Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr
                 80                  85                  90
```

```
gaa gac tac aag caa aac cat aca gaa gcg ctt aat ttt ttc aga ata      821
Glu Asp Tyr Lys Gln Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile
                 95                  100                 105
```

```
gcg gaa aaa agg ctg agc gtc att caa aat gaa att gaa aaa gcc gaa      869
Ala Glu Lys Arg Leu Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Glu
         110                 115                 120
```

```
ttt cat tat aaa atc ggt gtt ttg tat tac aac tta aaa gcg aca tgg      917
Phe His Tyr Lys Ile Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp
         125                 130                 135
```

```
ctg tcg att cac cac atc aac att gcc tca ggc atc ttc caa ggg tat      965
Leu Ser Ile His His Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr
140                 145                 150                 155
```

```
gac ggg tat gcc aag cgg gtc atc aac tgc aaa atg ctg atc ggg ctc     1013
Asp Gly Tyr Ala Lys Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu
                 160                 165                 170
```

```
aat tat att gac caa ttt aag ttt gcc gaa agt gaa gta ttg tta aag     1061
Asn Tyr Ile Asp Gln Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys
                 175                 180                 185
```

```
gaa gca att gaa aaa acc gaa aaa atc ggc gac caa tat ctt ttg cct       1109
Glu Ala Ile Glu Lys Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro
        190                 195                 200

tat acc tac tat aat atg ggc ttt ttg aag agt aag gaa gat aaa cac       1157
Tyr Thr Tyr Tyr Asn Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His
    205                 210                 215

gaa gaa gcg ctg aag tat tat aat aaa gct ttt gca atc aaa gac ttt       1205
Glu Glu Ala Leu Lys Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe
220             225                 230                 235

gaa acg aaa gcc aag tat gct tac ctt cta tgt gta tat gaa aac aca       1253
Glu Thr Lys Ala Lys Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr
            240                 245                 250

agg tct ctt ttc aaa acc aac gat ccc gac caa gct ttt aaa tgg atc       1301
Arg Ser Leu Phe Lys Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile
                255                 260                 265

gac aca ggc ttt aaa aaa gct caa gaa gtg aat agc gaa att ttc gaa       1349
Asp Thr Gly Phe Lys Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu
            270                 275                 280

tta aaa ttc aaa act tta tat aca tta cat tcc gat tgt cag aat aaa       1397
Leu Lys Phe Lys Thr Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys
        285                 290                 295

ctg gaa gta atc aag gac ttt att cac caa tta gaa gat aaa aaa gca       1445
Leu Glu Val Ile Lys Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala
300             305                 310                 315

tgg gtt gat ctg gag gaa ttg ctg atg gac gta gcg aat tac tat agg       1493
Trp Val Asp Leu Glu Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg
                320                 325                 330

gaa aat aag tta tac gaa gaa gcc ata tat ttc tac att aaa aca gac       1541
Glu Asn Lys Leu Tyr Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp
            335                 340                 345

aag gca agt aaa ctt gcc gga aga gga gga gaa taggatgaaa aaagtgttgt     1594
Lys Ala Ser Lys Leu Ala Gly Arg Gly Gly Glu
            350                 355

tagctgtatt tgtattaggc actgttttca gcttttcgtt tgcaaatcac gctcctgaag    1654

cggcttccca aagcaatgag atactttggg cttctcgtgg agcaggcggg tgactacatc    1714

ctcaaaatac ccattcagac atctgctgaa tgggtatttt gcactttaca ttcatattca    1774

ggagtgatcg atatgggaaa gaaagtactg ctgacaggat ttgaccccctt tgggggagaa   1834

acagtcaatc cgtcctggga agctgtaaaa cggctgaacg gagaggaagc agaaggcgtc    1894

tctatcgcag cggagcagat tccgaccgtt tttcatcatt cagcggccgt tttgaaaaaa    1954

gcgatcgaaa agcacaaacc cgatgtcgtc atttgcgcag ggcaagcagg cggcagggct    2014

catattacgc cggaacgcat cgcaatcaac atcgatgatg ctcgcattcc ggataatgaa    2074

gac                                                                   2077
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`<210> 34`

`<211> 358`

<212> PRT

<213> Bacillus licheniformis

<400> 34

Met Leu Asn Asp Trp Tyr Ile Leu Met Lys Lys Arg Asp Ile Ser Gly
1   5   10   15

Ser Ile Glu Met Lys Asp Asp Ile Asp Lys Ala Ile Glu Lys Met Glu
            20   25   30

Glu Asp His Asp Val Leu Leu Tyr Tyr Gln Met Leu Asp Phe Arg Leu
        35   40   45

Arg Leu Leu Leu Glu Asp Ile Ser Gln Ser Ser Thr Glu Lys Leu Glu
    50   55   60

Ala Ile Ser Phe Lys Asp Lys Asp Pro Lys Ser Thr Asp Asp Lys Leu
65   70   75   80

Asn Tyr Tyr Phe Tyr Leu Phe Lys Gly Ile Tyr Glu Asp Tyr Lys Gln
                85   90   95

Asn His Thr Glu Ala Leu Asn Phe Phe Arg Ile Ala Glu Lys Arg Leu
            100   105   110

Ser Val Ile Gln Asn Glu Ile Glu Lys Ala Glu Phe His Tyr Lys Ile
        115   120   125

Gly Val Leu Tyr Tyr Asn Leu Lys Ala Thr Trp Leu Ser Ile His His
    130   135   140

Ile Asn Ile Ala Ser Gly Ile Phe Gln Gly Tyr Asp Gly Tyr Ala Lys
145   150   155   160

Arg Val Ile Asn Cys Lys Met Leu Ile Gly Leu Asn Tyr Ile Asp Gln
                165   170   175

Phe Lys Phe Ala Glu Ser Glu Val Leu Leu Lys Glu Ala Ile Glu Lys
            180   185   190

Thr Glu Lys Ile Gly Asp Gln Tyr Leu Leu Pro Tyr Thr Tyr Tyr Asn
        195   200   205

Met Gly Phe Leu Lys Ser Lys Glu Asp Lys His Glu Glu Ala Leu Lys
    210   215   220

Tyr Tyr Asn Lys Ala Phe Ala Ile Lys Asp Phe Glu Thr Lys Ala Lys
225   230   235   240

Page 48

```
Tyr Ala Tyr Leu Leu Cys Val Tyr Glu Asn Thr Arg Ser Leu Phe Lys
             245             250                 255


Thr Asn Asp Pro Asp Gln Ala Phe Lys Trp Ile Asp Thr Gly Phe Lys
             260             265                 270


Lys Ala Gln Glu Val Asn Ser Glu Ile Phe Glu Leu Lys Phe Lys Thr
             275             280                 285


Leu Tyr Thr Leu His Ser Asp Cys Gln Asn Lys Leu Glu Val Ile Lys
     290             295             300


Asp Phe Ile His Gln Leu Glu Asp Lys Lys Ala Trp Val Asp Leu Glu
305             310             315                 320


Glu Leu Leu Met Asp Val Ala Asn Tyr Tyr Arg Glu Asn Lys Leu Tyr
             325             330                 335


Glu Glu Ala Ile Tyr Phe Tyr Ile Lys Thr Asp Lys Ala Ser Lys Leu
             340             345                 350


Ala Gly Arg Gly Gly Glu
         355
```

<210> 35

<211> 2101

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1598)

<223>

<400> 35

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aaaacagcat gggctaaaat gacgctggac aaagcagtgt ccttaggctt ggaggcaaat      60

gcatatttga aaagaaacac agacggaaaa gaactgagct gcagcccggc tggaggaaaa     120

ggaaaagtgc tcccgggggca gacatcctgt tatacaccga tggttgattt cgatccgcgt    180

tcttcatatg cgatgtagaa acattatcaa tccattaaca ggagctctca cttattccta     240

tacaagttcg tattcatatt tgaagaagta gtgtataaaa gcaccctttc agcaagggtg      300

cttttttgctg tcttatcagt cacggtttca cagctattga agagtcattt gacctaataa    360

aagagtggga aaagtggggg attcaggaaa ctgtgtaaaa tgaactatta ctattaattt     420

atacagggag gaaaatatag tatgatatga ataatgaata aaatacaaaa aaattgaata    480
```

Page 49

```
tcggaagaaa ggagctccat atg aac aag atc gcc gcg gaa gaa gtc gcc aac    533
                      Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn
                       1               5                   10


atc ctt aat aca tgg tac cgc gcc atc aga aga aat gat gct gaa cag    581
Ile Leu Asn Thr Trp Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln
             15                  20                  25


tcg atc cga ata ttt gaa gaa gtc aaa ccg atg ctg gca gag atg gag    629
Ser Ile Arg Ile Phe Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu
         30                  35                  40


gaa gac caa gag gtt tta atc tac tat tct ctg ctg gaa ctg cgg cat    677
Glu Asp Gln Glu Val Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His
     45                  50                  55


aaa atc atg ctg tat gat acg cgg gga aaa aag ata gaa cag caa gag    725
Lys Ile Met Leu Tyr Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu
 60                  65                  70                  75


gag tta acg aac ggc ggc agt gct gca tca cat atg aca tcc tat tac    773
Glu Leu Thr Asn Gly Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr
                 80                  85                  90


tac tac ctg ttt tca gga gct tat gaa gtg tat aaa aag aat tat gag    821
Tyr Tyr Leu Phe Ser Gly Ala Tyr Glu Val Tyr Lys Lys Asn Tyr Glu
             95                  100                 105


cag gcg atc agc ttc tat aaa att gcc gag aag aag ctt gct cat gta    869
Gln Ala Ile Ser Phe Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val
         110                 115                 120


cat gat gaa att gag gtg gcg caa ttt cac gat aaa gtc gga aag ctc    917
His Asp Glu Ile Glu Val Ala Gln Phe His Asp Lys Val Gly Lys Leu
     125                 130                 135


tac tat tac ttg ggc cag aat atc gtc tct tta aac cat acc cgg cag    965
Tyr Tyr Tyr Leu Gly Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln
140                 145                 150                 155


gcg atg gaa att ttc aag ggg cat ggc gac cat gat atg aac ctt gtt    1013
Ala Met Glu Ile Phe Lys Gly His Gly Asp His Asp Met Asn Leu Val
                 160                 165                 170


tcc act tat att acg atg gcc gga aat tat aca gag atg ggg aaa tat    1061
Ser Thr Tyr Ile Thr Met Ala Gly Asn Tyr Thr Glu Met Gly Lys Tyr
             175                 180                 185


aca gag gcg gaa gaa tat tta aca gaa gcc atc cat acg gta aga aaa    1109
Thr Glu Ala Glu Glu Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys
         190                 195                 200


gcc ggc gac tgt ttt aaa gaa atg cag ctc ctt cat aat ttt gcc ttg    1157
Ala Gly Asp Cys Phe Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu
         205                 210                 215


ctt tat gcg gcg atg gac aat tcg gaa aaa agc att cag ttt tta gaa    1205
Leu Tyr Ala Ala Met Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu
220                 225                 230                 235


atc gtt ttg gat gat caa gca tat gct gca tca gat tat tat ttc aat    1253
Ile Val Leu Asp Asp Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn
                 240                 245                 250


gct gtg ttt tta atg atc aaa gag ctg ttt aaa gtc gga gac cat aaa    1301
Ala Val Phe Leu Met Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys
             255                 260                 265
```

```
cgc gct gca gcc ttt tac aaa gaa ggg aag gaa agg tcg aaa tcc gcg      1349
Arg Ala Ala Ala Phe Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala
        270             275                 280

gcg aat aaa ata ttt gac gcc aaa atc gat att tta tat gcg gct tat      1397
Ala Asn Lys Ile Phe Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr
        285             290                 295

gca gga gat ggt gaa cag gcg gtt aaa gac tgc aaa gac aac att gaa      1445
Ala Gly Asp Gly Glu Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu
300             305                 310                 315

atc ctg ttt caa aca aag caa tac gac agc gcc aga gaa ctt tcg ctc      1493
Ile Leu Phe Gln Thr Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu
            320                 325                 330

tta acg gcc aat gtt tac aga tca aag tca ctt tat aaa gaa gcc gca      1541
Leu Thr Ala Asn Val Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala
            335                 340                 345

cat ttc ttt ttg gaa gcg att aaa gcg gaa gaa aaa atg aaa aaa gtg      1589
His Phe Phe Leu Glu Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val
            350                 355                 360

gag gga atg tgatgaaaaa actgttcatt gttgctgcga ttgctgccgt             1638
Glu Gly Met
        365

cgtatgttcg ggatggtttg cggcagaaac tcactgggca tccggcgaca tgcaggttgc   1698

tgaaaagatg gtcggttaaa tcgaatactc ggaacaaata tgaacatccg ctcctgagca   1758

tcagggcgga tttttttggg aaggtaaagt aaattaaggc ataagaaacg cggttagaca   1818

atgaacactt cttcaccact atttagggtg gtcaacctaa acaaaggtac gaaacctgtg   1878

ctgactactt ttactccgat gtcctttcag ctattcttgt cagtaagatc attccccatc   1938

tcttcaacgc ctcaggcatc acctattaaa aaaatcataa ttgaaacttg tcagcaaata   1998

tgttgcataa cacgaggatg tttccacaat aattaaacat taagactttt ttgacttcca   2058

gaaggaagaa caagatattt atgtaaaatc actcttttat tca                     2101
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<210> 36

<211> 366

<212> PRT

<213> Bacillus licheniformis

<400> 36

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Met Asn Lys Ile Ala Ala Glu Glu Val Ala Asn Ile Leu Asn Thr Trp
1               5                   10                  15


Tyr Arg Ala Ile Arg Arg Asn Asp Ala Glu Gln Ser Ile Arg Ile Phe
                20              25                  30


Glu Glu Val Lys Pro Met Leu Ala Glu Met Glu Glu Asp Gln Glu Val
        35              40                  45
```

```
Leu Ile Tyr Tyr Ser Leu Leu Glu Leu Arg His Lys Ile Met Leu Tyr
    50              55              60

Asp Thr Arg Gly Lys Lys Ile Glu Gln Gln Glu Glu Leu Thr Asn Gly
65              70              75              80

Gly Ser Ala Ala Ser His Met Thr Ser Tyr Tyr Tyr Tyr Leu Phe Ser
            85              90              95

Gly Ala Tyr Glu Val Tyr Lys Lys Asn Tyr Glu Gln Ala Ile Ser Phe
        100             105             110

Tyr Lys Ile Ala Glu Lys Lys Leu Ala His Val His Asp Glu Ile Glu
    115             120             125

Val Ala Gln Phe His Asp Lys Val Gly Lys Leu Tyr Tyr Tyr Leu Gly
    130             135             140

Gln Asn Ile Val Ser Leu Asn His Thr Arg Gln Ala Met Glu Ile Phe
145             150             155             160

Lys Gly His Gly Asp His Asp Met Asn Leu Val Ser Thr Tyr Ile Thr
            165             170             175

Met Ala Gly Asn Tyr Thr Glu Met Gly Lys Tyr Thr Glu Ala Glu Glu
            180             185             190

Tyr Leu Thr Glu Ala Ile His Thr Val Arg Lys Ala Gly Asp Cys Phe
    195             200             205

Lys Glu Met Gln Leu Leu His Asn Phe Ala Leu Leu Tyr Ala Ala Met
    210             215             220

Asp Asn Ser Glu Lys Ser Ile Gln Phe Leu Glu Ile Val Leu Asp Asp
225             230             235             240

Gln Ala Tyr Ala Ala Ser Asp Tyr Tyr Phe Asn Ala Val Phe Leu Met
            245             250             255

Ile Lys Glu Leu Phe Lys Val Gly Asp His Lys Arg Ala Ala Ala Phe
            260             265             270

Tyr Lys Glu Gly Lys Glu Arg Ser Lys Ser Ala Ala Asn Lys Ile Phe
    275             280             285

Asp Ala Lys Ile Asp Ile Leu Tyr Ala Ala Tyr Ala Gly Asp Gly Glu
    290             295             300

Gln Ala Val Lys Asp Cys Lys Asp Asn Ile Glu Ile Leu Phe Gln Thr
305             310             315             320
```

Page 52

```
Lys Gln Tyr Asp Ser Ala Arg Glu Leu Ser Leu Leu Thr Ala Asn Val
            325                 330                 335


Tyr Arg Ser Lys Ser Leu Tyr Lys Glu Ala Ala His Phe Phe Leu Glu
            340                 345                 350


Ala Ile Lys Ala Glu Glu Lys Met Lys Lys Val Glu Gly Met
            355                 360                 365
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<210> 37

<211> 1936

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (384)..(1433)

<223>

<400> 37

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taatgaagca aaaccgggga gcaaatgggc gattggaaca gagatgaacc ttgtttcacg      60

catcattcaa gaacatcctg ataaacaaat cgaatccctt aaccctgata tgtgtccttg     120

tttgacaatg aacagaatcg acatgccgca tttgctgtgg tcgctggagc agatcgacaa     180

aggtgaaccg acaggcgtga tcaaagtgga tcaagatatt gcaaaagatg ccattcttgc     240

gctgaatcgg atgttaacga tccgttaact ttttggagaa caagttttta tcataacccc     300

tccgctatgc gcataaattt gtggagaagc atatttgtta ttctcatctg ttcgttcacg     360

tttttgcata ggaggggaaa acg ttg aaa att cat att gtc caa aag ggc gat   413
                         Leu Lys Ile His Ile Val Gln Lys Gly Asp
                          1               5                   10

tct ctg gaa aaa atc gcg gaa aga tat gaa gtg gac ttt gaa gaa ctg      461
Ser Leu Glu Lys Ile Ala Glu Arg Tyr Glu Val Asp Phe Glu Glu Leu
                 15              20                  25

aaa aag ctg aat tcg cag ctg agc aat cca gac ttg atc atg ccg ggc      509
Lys Lys Leu Asn Ser Gln Leu Ser Asn Pro Asp Leu Ile Met Pro Gly
            30              35                  40

atg aaa atc aaa gta ccg tca ggg gga gtg ccg gtc aaa aaa gaa gaa      557
Met Lys Ile Lys Val Pro Ser Gly Gly Val Pro Val Lys Lys Glu Glu
        45              50                  55

cag ctc aat atg cga aag gaa tta ccg aaa aaa cag cag gaa cat cca      605
Gln Leu Asn Met Arg Lys Glu Leu Pro Lys Lys Gln Gln Glu His Pro
        60              65                  70

ttt gca aaa gaa aag ccg aaa agc aag ctt gat gtt gaa gat ata aaa      653
```

Page 53

```
Phe Ala Lys Glu Lys Pro Lys Ser Lys Leu Asp Val Glu Asp Ile Lys
75              80              85                  90

ccg aaa gaa aag cct tcg gtt cct tat gtt ccg cct gtc ccg aac atc    701
Pro Lys Glu Lys Pro Ser Val Pro Tyr Val Pro Pro Val Pro Asn Ile
                95              100                 105

gga caa tca agt ttg cct gaa ggc gac att tcg aat ttg tat caa agc    749
Gly Gln Ser Ser Leu Pro Glu Gly Asp Ile Ser Asn Leu Tyr Gln Ser
                110             115                 120

gtc aat cag ctt cat cag ccg tac gta cct cca aaa cct tat gaa cat    797
Val Asn Gln Leu His Gln Pro Tyr Val Pro Pro Lys Pro Tyr Glu His
            125             130             135

caa gag aaa ggc ccc aac atg tat aat cca tgg aca aat gag gag gaa    845
Gln Glu Lys Gly Pro Asn Met Tyr Asn Pro Trp Thr Asn Glu Glu Glu
        140             145             150

aac cat atg gaa aat gtc aat tat ccg aat gtt ccg cag ccg cca aat    893
Asn His Met Glu Asn Val Asn Tyr Pro Asn Val Pro Gln Pro Pro Asn
155             160             165                 170

gtc ggt gca gca ggt gat gaa aat aag cag ttt cac ggc atg ccg aat    941
Val Gly Ala Ala Gly Asp Glu Asn Lys Gln Phe His Gly Met Pro Asn
            175             180             185

gta gct gca gcg gga tat cat cac cat cca tat cct tat ccg ttc tat    989
Val Ala Ala Ala Gly Tyr His His His Pro Tyr Pro Tyr Pro Phe Tyr
            190             195             200

cct gga ggc tgc tgg att cct gtt tca ccg gtg ctg cct gga tcg gga    1037
Pro Gly Gly Cys Trp Ile Pro Val Ser Pro Val Leu Pro Gly Ser Gly
            205             210             215

ttg tgc cat cct tgg tat cca tat cct gct caa atg cct tat atg cat    1085
Leu Cys His Pro Trp Tyr Pro Tyr Pro Ala Gln Met Pro Tyr Met His
    220             225             230

cag cct agc tat gta tct cct gct gaa tat gac gat gat gac aac atg    1133
Gln Pro Ser Tyr Val Ser Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met
235             240             245                 250

ggg cat gac aat gcc ggt cat cac gga tac cat cat cag ccg atg act    1181
Gly His Asp Asn Ala Gly His His Gly Tyr His His Gln Pro Met Thr
                255             260             265

gcc ccg gca tat gcg cct tac cag ccg ttc ccg gga ttt gca ccg cca    1229
Ala Pro Ala Tyr Ala Pro Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro
            270             275             280

aac gtc ggt cac gcc ggg gac cct aat atg gca cac ggc aaa gaa gat    1277
Asn Val Gly His Ala Gly Asp Pro Asn Met Ala His Gly Lys Glu Asp
            285             290             295

gac tgc ggg tgc ggg ccg ggc caa ttc ccg gga ggt ttt cca ggt gcg    1325
Asp Cys Gly Cys Gly Pro Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala
    300             305             310

gcg cca tat gga cag atg ccg caa atg gga gct ccg tac ggt atg ggg    1373
Ala Pro Tyr Gly Gln Met Pro Gln Met Gly Ala Pro Tyr Gly Met Gly
315             320             325             330

gga tac gga cag cag cct gca ggg gga cag atg ttt aac aga ccg gaa    1421
Gly Tyr Gly Gln Gln Pro Ala Gly Gly Gln Met Phe Asn Arg Pro Glu
            335             340             345

gat gat gaa gac tgattcggaa tgggacgatg atctatcgtt cctttttat       1473
Asp Asp Glu Asp
```

Asp Asp Glu Asp
              350

tgtggaccgc tataaacatt ttcatgctat ttaacgggaa tgtctataac tgtcaagggt   1533

aactcttcgc atcccgcaca tcctaaaaaa gagcgcaatg ctcaaattca gcggttttca   1593

cgggggggtac taccattgga cagcaagctg aaagtgtttt cggggatttt gcttttgaca   1653

gcaggtctat ctgcatgcgg aacgaacgac gctatagata atggaaacaa tacgcgcccg   1713

atcggatatt atctcaaatg atgcagatcg taatgcaggg tcttgataat gacggccctg   1773

ttacagaaat gcttgaaaac atgaacggga gacacggtgc aacaaacgta aacaatcgag   1833

cgggaaacgg caatcccgtt ccaacaggcg atggaactta cagccgggga gacatgaatt   1893

atcacaacca tttggtgaat acggcggata caggctatga cag   1936

<210>   38

<211>   350

<212>   PRT

<213>   Bacillus licheniformis

<400>   38

Leu Lys Ile His Ile Val Gln Lys Gly Asp Ser Leu Glu Lys Ile Ala
1   5   10   15

Glu Arg Tyr Glu Val Asp Phe Glu Glu Leu Lys Lys Leu Asn Ser Gln
            20   25   30

Leu Ser Asn Pro Asp Leu Ile Met Pro Gly Met Lys Ile Lys Val Pro
        35   40   45

Ser Gly Gly Val Pro Val Lys Lys Glu Glu Gln Leu Asn Met Arg Lys
    50   55   60

Glu Leu Pro Lys Lys Gln Gln Glu His Pro Phe Ala Lys Glu Lys Pro
65   70   75   80

Lys Ser Lys Leu Asp Val Glu Asp Ile Lys Pro Lys Glu Lys Pro Ser
                85   90   95

Val Pro Tyr Val Pro Pro Val Pro Asn Ile Gly Gln Ser Ser Leu Pro
            100   105   110

Glu Gly Asp Ile Ser Asn Leu Tyr Gln Ser Val Asn Gln Leu His Gln
            115   120   125

Pro Tyr Val Pro Pro Lys Pro Tyr Glu His Gln Glu Lys Gly Pro Asn
        130   135   140

```
Met Tyr Asn Pro Trp Thr Asn Glu Glu Glu Asn His Met Glu Asn Val
145                 150             155                 160

Asn Tyr Pro Asn Val Pro Gln Pro Pro Asn Val Gly Ala Ala Gly Asp
                165             170                 175

Glu Asn Lys Gln Phe His Gly Met Pro Asn Val Ala Ala Ala Gly Tyr
            180             185                 190

His His His Pro Tyr Pro Tyr Pro Phe Tyr Pro Gly Gly Cys Trp Ile
            195             200                 205

Pro Val Ser Pro Val Leu Pro Gly Ser Gly Leu Cys His Pro Trp Tyr
    210             215                 220

Pro Tyr Pro Ala Gln Met Pro Tyr Met His Gln Pro Ser Tyr Val Ser
225                 230             235                 240

Pro Ala Glu Tyr Asp Asp Asp Asp Asn Met Gly His Asp Asn Ala Gly
                245             250                 255

His His Gly Tyr His His Gln Pro Met Thr Ala Pro Ala Tyr Ala Pro
                260             265                 270

Tyr Gln Pro Phe Pro Gly Phe Ala Pro Pro Asn Val Gly His Ala Gly
        275             280                 285

Asp Pro Asn Met Ala His Gly Lys Glu Asp Asp Cys Gly Cys Gly Pro
    290             295                 300

Gly Gln Phe Pro Gly Gly Phe Pro Gly Ala Ala Pro Tyr Gly Gln Met
305                 310             315                 320

Pro Gln Met Gly Ala Pro Tyr Gly Met Gly Gly Tyr Gly Gln Gln Pro
            325             330                 335

Ala Gly Gly Gln Met Phe Asn Arg Pro Glu Asp Asp Glu Asp
            340             345                 350
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<210> 39

<211> 2027

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1526)

<223>

<400> 39

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tcaacctggc ataagcaatt gaaaatccgg accggcatca ccaatgcccg tccgggtttt     120

ttgtttatct gaatgatccc ggctgcggcg gagataatac atgtgaccaa ttgttagaaa     180

gggggattct gatatgccta ggcagccatt caaactggga gatgaggtgt atgtcattta     240

ccggaatccg catgcagcga atgtggcgca tataaaggaa gctgaagtcg ttgatcatcc     300

gcttcacgaa ggcgaactgg cattgtttat gtatgataca tatcacgcct tgccgaaga     360

tgatgccgtt ttttcttcat atgaagaggc ggaacggctt taccgtgaat tatttgacgg     420

gatatgaaga cattaccggt atatcacatc ctctaaatgc aaaaagtaat ggaaatatgc     480

aaaggatgtg tctgtttcca atg gta aaa ccg ttt gtt ccc caa ctc gtc tat     533
                        Met Val Lys Pro Phe Val Pro Gln Leu Val Tyr
                         1               5                  10
```

```
att gaa ccg aga gcc ctg gaa tat ccg ctt gga aaa gag ctg agg gat      581
Ile Glu Pro Arg Ala Leu Glu Tyr Pro Leu Gly Lys Glu Leu Arg Asp
              15                  20                  25
```

```
aaa ttt tca aac atg gga ctt gag atc agg gaa aca act tca cac aac      629
Lys Phe Ser Asn Met Gly Leu Glu Ile Arg Glu Thr Thr Ser His Asn
              30                  35                  40
```

```
cag gtg agg aat atc ccg ggg gaa ggc cac ctg caa aaa tac aga aat      677
Gln Val Arg Asn Ile Pro Gly Glu Gly His Leu Gln Lys Tyr Arg Asn
      45                  50                  55
```

```
gcg aaa tcc act ttg gtg atc ggc gtc aga aaa aca ttg aag ttc gat      725
Ala Lys Ser Thr Leu Val Ile Gly Val Arg Lys Thr Leu Lys Phe Asp
60                  65                  70                  75
```

```
tcg tca aaa ccg tcc gca gaa tac gcg atc ccg ttt gca aca ggg tgt      773
Ser Ser Lys Pro Ser Ala Glu Tyr Ala Ile Pro Phe Ala Thr Gly Cys
                  80                  85                  90
```

```
atg ggt cac tgt cat tac tgc tac ctg caa acg aca atg ggc agc aag      821
Met Gly His Cys His Tyr Cys Tyr Leu Gln Thr Thr Met Gly Ser Lys
              95                  100                 105
```

```
ccg tat atc aga acg tac gtc aat gtg gag gaa ata ctt gag cag gcg      869
Pro Tyr Ile Arg Thr Tyr Val Asn Val Glu Glu Ile Leu Glu Gln Ala
              110                 115                 120
```

```
gat caa tat ata aaa gaa agg gct ccc gaa gat acg cgg ttt gaa gct      917
Asp Gln Tyr Ile Lys Glu Arg Ala Pro Glu Asp Thr Arg Phe Glu Ala
      125                 130                 135
```

```
tcc tgc aca tcc gat atc gtc gga att gac cat ttg aca cat acg tta      965
Ser Cys Thr Ser Asp Ile Val Gly Ile Asp His Leu Thr His Thr Leu
140                 145                 150                 155
```

```
aaa cgc gcc att gag cat ttc ggt caa acc gac cat ggt aag ctg cgt     1013
Lys Arg Ala Ile Glu His Phe Gly Gln Thr Asp His Gly Lys Leu Arg
              160                 165                 170
```

```
ttc gtg aca aaa ttt cat cat gtc gac cat ttg ctc gat gcc aag cac     1061
Phe Val Thr Lys Phe His His Val Asp His Leu Leu Asp Ala Lys His
              175                 180                 185
```

```
aac gga aaa acg cgc ttc cgc ttc agc gtg aat gcc gaa tat gtc att    1109
Asn Gly Lys Thr Arg Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile
        190                 195                 200

aaa agc ttt gaa ccc ggc aca tcc ccg ttg gat aaa cgg atc gaa gcc    1157
Lys Ser Phe Glu Pro Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala
        205                 210                 215

gcc gtg aaa gta gcg gaa gcg ggc tat ccg ctc ggt ttt atc atc gct    1205
Ala Val Lys Val Ala Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala
220                 225                 230                 235

ccg att tat att cat gac ggc tgg cag gaa ggc tac aga gtt ctg ctg    1253
Pro Ile Tyr Ile His Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu
                240                 245               .  250

gaa aag ctc gat cgt gcg ctg ccg cag cat gcg agg cgc gac atc acc    1301
Glu Lys Leu Asp Arg Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr
                255                 260                 265

ttt gaa atg atc cag cat aga ttc acg aag ccg gca aag aga gtc att    1349
Phe Glu Met Ile Gln His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile
                270                 275                 280

gaa aaa aac tat cca aag aca aag ctc gaa ctg gat gaa gaa aaa cgg    1397
Glu Lys Asn Tyr Pro Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg
        285                 290                 295

cgc tat aaa tgg ggc aga tac ggg att ggc aaa tac att tat cag aag    1445
Arg Tyr Lys Trp Gly Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys
300                 305                 310                 315

gat gaa gaa gca gag ctt cgc agc gcc ctt gaa tcg tat atc gac aac    1493
Asp Glu Glu Ala Glu Leu Arg Ser Ala Leu Glu Ser Tyr Ile Asp Asn
                320                 325                 330

tat ttt ccc gaa gca aaa atc gaa tat ttc aca taacagagct ttagttgata  1546
Tyr Phe Pro Glu Ala Lys Ile Glu Tyr Phe Thr
                335                 340

aagctctgtt ttttgttttg aaaacattat gttaaaaaag gattttttcca ctccattaac  1606

accgcataat caagcgattc ctcatcttca atgtagccgg gaatcacaca aactggagag  1666

cgtccgcaat gaagcaggaa cgagagcact ggatcgcgct tttccccgtc caatacagct  1726

tgaacatact gttcgggcgt catttcttca gccgacttgt gataatgggg aatccgtccg  1786

ccgccaatga gacgcttgag cccttttaaag accgtcagtt catacatgga ttgcatcagc  1846

cgcattccga tgccgagttt tcgatagtcg ggggacacgg aaatatcgac gacataaagg  1906

gagtttccat cgttttgatg tgtgccgata tacccgttgt ccgtcacttc atcccagctg  1966

tggtgcggat gatgcggatc aaaatcagcc atgagcgctg tcatcgaacc gatgatgcgg  2026

c                                                                   2027
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<210> 40

<211> 342

<212> PRT

<213> Bacillus licheniformis

<400> 40

Met Val Lys Pro Phe Val Pro Gln Leu Val Tyr Ile Glu Pro Arg Ala
1   5   10   15

Leu Glu Tyr Pro Leu Gly Lys Glu Leu Arg Asp Lys Phe Ser Asn Met
            20   25   30

Gly Leu Glu Ile Arg Glu Thr Thr Ser His Asn Gln Val Arg Asn Ile
        35   40   45

Pro Gly Glu Gly His Leu Gln Lys Tyr Arg Asn Ala Lys Ser Thr Leu
    50   55   60

Val Ile Gly Val Arg Lys Thr Leu Lys Phe Asp Ser Ser Lys Pro Ser
65   70   75   80

Ala Glu Tyr Ala Ile Pro Phe Ala Thr Gly Cys Met Gly His Cys His
            85   90   95

Tyr Cys Tyr Leu Gln Thr Thr Met Gly Ser Lys Pro Tyr Ile Arg Thr
            100   105   110 ·

Tyr Val Asn Val Glu Glu Ile Leu Glu Gln Ala Asp Gln Tyr Ile Lys
        115   120   125

Glu Arg Ala Pro Glu Asp Thr Arg Phe Glu Ala Ser Cys Thr Ser Asp
    130   135   140

Ile Val Gly Ile Asp His Leu Thr His Thr Leu Lys Arg Ala Ile Glu
145   150   155   160

His Phe Gly Gln Thr Asp His Gly Lys Leu Arg Phe Val Thr Lys Phe
            165   170   175

His His Val Asp His Leu Leu Asp Ala Lys His Asn Gly Lys Thr Arg
        180   185   190

Phe Arg Phe Ser Val Asn Ala Glu Tyr Val Ile Lys Ser Phe Glu Pro
    195   200   205

Gly Thr Ser Pro Leu Asp Lys Arg Ile Glu Ala Ala Val Lys Val Ala
    210   215   220

Glu Ala Gly Tyr Pro Leu Gly Phe Ile Ile Ala Pro Ile Tyr Ile His
225   230   235   240

Asp Gly Trp Gln Glu Gly Tyr Arg Val Leu Leu Glu Lys Leu Asp Arg
            245   250   255

Page 59

Ala Leu Pro Gln His Ala Arg Arg Asp Ile Thr Phe Glu Met Ile Gln
         260   265   270

His Arg Phe Thr Lys Pro Ala Lys Arg Val Ile Glu Lys Asn Tyr Pro
     275   280   285

Lys Thr Lys Leu Glu Leu Asp Glu Glu Lys Arg Arg Tyr Lys Trp Gly
   290   295   300

Arg Tyr Gly Ile Gly Lys Tyr Ile Tyr Gln Lys Asp Glu Glu Ala Glu
305   310   315   320

Leu Arg Ser Ala Leu Glu Ser Tyr Ile Asp Asn Tyr Phe Pro Glu Ala
        325   330   335

Lys Ile Glu Tyr Phe Thr
      340

<210> 41

<211> 905

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(905)

<223>

<400> 41
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tccatttcat cgaaagacgg aaccgatttg atcgccgtca caatcaatgc ccctgacgac 120
tggaatgatc atatgaacat gttcaactat gtattcggcc agtacaaaac atatatcatc 180
gccaaaaaag gcgagattcc gaaattaaaa gactcttttt acggacatac agcttttatt 240
aaacgggatg tcacatatct tttaaacgaa gaggaaaaag aagatgtgaa ggttgatatc 300
gagcttcttg aaccgaaaaa atcatggcgt aaaaacaaaa aagaaatccc ggacatcatc 360
ggagaaatga acgtcatgtt cgacggaaaa acgattgcaa gcgtaccgat ctattatgaa 420
aacgagcgaa acaaaaatcc gaaaaaatcg tttttcgaga cctttcaatc cgtattccaa 480
aaagcggcgg cggttcatc atg gtc aat ata atc tgg gtc ggc tta acg gtg 533
                     Met Val Asn Ile Ile Trp Val Gly Leu Thr Val
                     1   5   10

atc ggt atg gtg ttt gcg ctt ttc aac ggc acg gtt cag gaa gtt aat 581
Ile Gly Met Val Phe Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn
        15   20   25

```
gaa gct gta ttt aaa gga tcg aag gaa gcc gtc acg att gtg atc gga        629
Glu Ala Val Phe Lys Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly
        30                      35                  40

ctg atg agc gtc ctt gtt ttt tgg ctg ggg gtg atg aaa atc gct gaa        677
Leu Met Ser Val Leu Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu
    45                      50                  55

cag tcc ggg ctt ctc gaa aaa ttc agc agg ctg tgc cgg ccg ttc att        725
Gln Ser Gly Leu Leu Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile
60                  65                  70                  75

tcg aag ctg ttt ccc gag atc cct ccg gat cat ccg gcg atg gga tat        773
Ser Lys Leu Phe Pro Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr
                80                  85                  90

att tta tcc aat tta atg gcc aac ttt ttc gga ttg ggc aat gca gcg        821
Ile Leu Ser Asn Leu Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala
                95                  100                 105

aca ccg ctc ggt att aaa gcg atg gaa cag atg aag gcg ctc aac cgg        869
Thr Pro Leu Gly Ile Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg
        110                     115                 120

aac cgc agg gaa gcg agc cgc tca atg cac cca ggc                        905
Asn Arg Arg Glu Ala Ser Arg Ser Met His Pro Gly
        125                     130                 135
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<210>   42

<211>   135

<212>   PRT

<213>   Bacillus licheniformis

<400>   42

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Met Val Asn Ile Ile Trp Val Gly Leu Thr Val Ile Gly Met Val Phe
1               5                   10              15

Ala Leu Phe Asn Gly Thr Val Gln Glu Val Asn Glu Ala Val Phe Lys
            20                  25                  30

Gly Ser Lys Glu Ala Val Thr Ile Val Ile Gly Leu Met Ser Val Leu
        35                  40                  45

Val Phe Trp Leu Gly Val Met Lys Ile Ala Glu Gln Ser Gly Leu Leu
    50                  55                  60

Glu Lys Phe Ser Arg Leu Cys Arg Pro Phe Ile Ser Lys Leu Phe Pro
65                  70                  75                  80

Glu Ile Pro Pro Asp His Pro Ala Met Gly Tyr Ile Leu Ser Asn Leu
                85                  90                  95

Met Ala Asn Phe Phe Gly Leu Gly Asn Ala Ala Thr Pro Leu Gly Ile
            100                 105                 110
```

Lys Ala Met Glu Gln Met Lys Ala Leu Asn Arg Asn Arg Arg Glu Ala
        115   120   125

Ser Arg Ser Met His Pro Gly
    130   135

<210> 43

<211> 1568

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1076)

<223>

<220>

<221> CDS

<222> (1112)..(1567)

<223>

<400> 43
gattagatct tcagtttttt gcatctaaaa aaggagtagg ttcaacgaaa aacggacgtg   60

actctgaagc gaagcgccta ggtgctaaac gtgcagacgg tcaattcgta tctggccgtt   120

caatccttta tcgtcagcgc ggaacaaaaa tctatccaag tgaaaacgtt gggcgcggcc   180

gatattacac tctatttgca aaagtcgacg gaactgttaa attcgaacct ttcggccgta   240

cccccaaaaa agtgagcgta tatcctgtag cctaaccttt aaacgaaact ccggtcgttc   300

tgaccggagt tttttacatt cagcaccatg acttgcttaa aacaccttcc cgacgcctaa   360

ataaggccgg gtttccgctc tgattctgct tcgttaaagt atataaacgt gtttcattta   420

tactgccttc tctgttataa ttcaaagtac aaactgaatc agactcctaa aagagagacc   480

aaacgattgg gagtgccaaa atg gaa gaa act tcg aaa aaa cga gaa aag aat   533
                        Met Glu Glu Thr Ser Lys Lys Arg Glu Lys Asn
                         1   5   10

atg gac gat aag gct ttg acc cat gag ctt atc cat ctg ctc agc cac   581
Met Asp Asp Lys Ala Leu Thr His Glu Leu Ile His Leu Leu Ser His
            15   20   25

tca agg cac gac tgg atg aat aaa ctg caa ttg att aaa gga aac tta   629
Ser Arg His Asp Trp Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu
        30   35   40

```
aca tta aaa aag tat gac cgc gta ttt gaa att atc gat gaa gtg gtc      677
Thr Leu Lys Lys Tyr Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val
    45              50              55

atc gaa gct cag cat gaa tca aag ctt tca aac ctt aga atc ccg cgc      725
Ile Glu Ala Gln His Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg
60              65              70              75

gcg gcg tat gag ctg ctt aca ttt aac tgg atg gcc cat tcg ctg acg      773
Ala Ala Tyr Glu Leu Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr
            80              85              90

ctt gaa tat gag gtg atc ggt caa gtc aag gat ttg tca gct tat gaa      821
Leu Glu Tyr Glu Val Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu
                95              100             105

gaa agg ctc gtc gtt ctc atc aga aag ctg ttt ggg att ttt gac gat      869
Glu Arg Leu Val Val Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp
        110             115             120

gcc gtt ttg aaa ggc agc gac aat cat ctg acg atc acg ctg cag acg      917
Ala Val Leu Lys Gly Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr
    125             130             135

gac ggt ccg gac gac cgc ctc gtc atc ttt ctc gat ttc cac ggc gta      965
Asp Gly Pro Asp Asp Arg Leu Val Ile Phe Leu Asp Phe His Gly Val
140             145             150             155

ttc aca aag ctg acc ggt atc aaa gac ttt cat cat tca ctg gcc gac      1013
Phe Thr Lys Leu Thr Gly Ile Lys Asp Phe His His Ser Leu Ala Asp
                160             165             170

ttt tat gaa atc aag cgg ttt gat gta aca gac cgt gag tgc atc gcc      1061
Phe Tyr Glu Ile Lys Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala
                175             180             185

gaa att cat atc aag taaagcggtt ttttaggaat agaacggagg acatt atg      1114
Glu Ile His Ile Lys                                            Met
        190

ttt gtt gat cag gtg aaa ata tac gta aaa ggc gga gac gga ggc aac      1162
Phe Val Asp Gln Val Lys Ile Tyr Val Lys Gly Gly Asp Gly Gly Asn
    195             200             205

ggt atg gtt gct ttc cgc cgc gaa aaa tat gtg cca aaa gga ggc cct      1210
Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly Pro
210             215             220             225

gcc gga ggt gac ggc gga aaa ggc gga gac gtc gtt ttc aaa gtt gac      1258
Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val Asp
                230             235             240

gaa ggt ctc agc acg ctg atg gat ttt aga tat caa aga cat ttt aag      1306
Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe Lys
            245             250             255

gca gcg cgc gga gaa cac ggc atg tct aaa aac cag cac ggc cga aat      1354
Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg Asn
        260             265             270

gcc gaa gac atg gtt gtg aaa gtc ccg ccc ggc acg gtt gtc att gac      1402
Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile Asp
    275             280             285

gat gat aca aaa cag gtc atc gct gat tta acg gag cac gga cag gaa      1450
Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln Glu
290             295             300             305
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Page 63

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gcc gtc atc gca aaa ggg gga cgc ggc gga cgg ggc aat aca cgt ttt      1498
Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg Phe
                310                 315                 320

gcg acg cct gcc aac ccg gcg ccg cag ctt tct gaa aac ggc gaa ccc      1546
Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu Pro
                325                 330                 335

ggc aag gag cgc tat att gtt c                                        1568
Gly Lys Glu Arg Tyr Ile Val
                340
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<211> 192

<212> PRT

<213> Bacillus licheniformis

<400> 44

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Leu Thr His Glu Leu Ile His Leu Leu Ser His Ser Arg His Asp Trp
                20                  25                  30

Met Asn Lys Leu Gln Leu Ile Lys Gly Asn Leu Thr Leu Lys Lys Tyr
        35                  40                  45

Asp Arg Val Phe Glu Ile Ile Asp Glu Val Val Ile Glu Ala Gln His
        50                  55                  60

Glu Ser Lys Leu Ser Asn Leu Arg Ile Pro Arg Ala Ala Tyr Glu Leu
65                  70                  75                  80

Leu Thr Phe Asn Trp Met Ala His Ser Leu Thr Leu Glu Tyr Glu Val
                85                  90                  95

Ile Gly Gln Val Lys Asp Leu Ser Ala Tyr Glu Glu Arg Leu Val Val
                100                 105                 110

Leu Ile Arg Lys Leu Phe Gly Ile Phe Asp Asp Ala Val Leu Lys Gly
            115                 120                 125

Ser Asp Asn His Leu Thr Ile Thr Leu Gln Thr Asp Gly Pro Asp Asp
        130                 135                 140

Arg Leu Val Ile Phe Leu Asp Phe His Gly Val Phe Thr Lys Leu Thr
145                 150                 155                 160

Gly Ile Lys Asp Phe His His Ser Leu Ala Asp Phe Tyr Glu Ile Lys
                165                 170                 175
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Page 64

Arg Phe Asp Val Thr Asp Arg Glu Cys Ile Ala Glu Ile His Ile Lys
              180   185   190

<210> 45

<211> 152

<212> PRT

<213> Bacillus licheniformis

<400> 45

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Asn Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Lys Gly Gly
            20   25   30

Pro Ala Gly Gly Asp Gly Gly Lys Gly Gly Asp Val Val Phe Lys Val
        35   40   45

Asp Glu Gly Leu Ser Thr Leu Met Asp Phe Arg Tyr Gln Arg His Phe
    50   55   60

Lys Ala Ala Arg Gly Glu His Gly Met Ser Lys Asn Gln His Gly Arg
65   70   75   80

Asn Ala Glu Asp Met Val Val Lys Val Pro Pro Gly Thr Val Val Ile
                85   90   95

Asp Asp Asp Thr Lys Gln Val Ile Ala Asp Leu Thr Glu His Gly Gln
            100   105   110

Glu Ala Val Ile Ala Lys Gly Gly Arg Gly Gly Arg Gly Asn Thr Arg
        115   120   125

Phe Ala Thr Pro Ala Asn Pro Ala Pro Gln Leu Ser Glu Asn Gly Glu
    130   135   140

Pro Gly Lys Glu Arg Tyr Ile Val
145   150

<210> 46

<211> 1849

<212> DNA

<213> Bacillus licheniformis

<220>

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<222> (501)..(1346)

<223>

<400> 46

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agtccggctg aaaagggctt tggaatcggt caaacaaaac tatgatttca tgattattga     120

ctgcccgccg tcattagggc tgcttacaat caatgcgctt acggcttccg attccgtcgt     180

gattccggtc cagtgcgagt attatgcgct ggaagggctg agccagctgc tcaactctgt     240

ccggctcgtg caaaaacatt aaatacgga tctgatgatc gacggcgtat tgctgacaat      300

gcttgatgca agaacgaatt taggcataca ggtcatcgaa gaagtgaaaa agtacttccg     360

cgataaagta tacaaaacgg ttatcccccg gaatgtccgg ctcagtgaag cgccgagtca     420

tggaaagccg atcattttat atgatccccg ttccagagga gcggaagtct atttagaatt     480

agcaaaggaa gtggctgcga atg cct aaa ggt ctc gga aaa ggg att aat gca     533
                         Met Pro Lys Gly Leu Gly Lys Gly Ile Asn Ala
                         1               5                   10

ttg ttt tca aat gtt gat tta tcc gaa gaa acg gtt gag gaa atc aag      581
Leu Phe Ser Asn Val Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys
            15              20                  25

ctg caa gac ttg cgg ccc aac cct tat cag cca aga aaa acg ttt gat      629
Leu Gln Asp Leu Arg Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp
        30                  35                  40

gac caa tcg tta aaa gat ttg aag gag tcc att ttg cag cac ggt gtt      677
Asp Gln Ser Leu Lys Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val
    45                  50                  55

ttg cag ccc atc atc gtc aga aag tca att aaa ggc tat gac att gtg      725
Leu Gln Pro Ile Ile Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val
60                  65                  70                  75

gcc gga gaa cgc cgt ttc cgg gct gct gaa aag gcc gga ttg gaa acc      773
Ala Gly Glu Arg Arg Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr
                80                  85                  90

att cct gcg att gtg cgc gag ctg tcg gaa tcc ctg atg atg gag att      821
Ile Pro Ala Ile Val Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile
                95                  100                 105

gcc cta ttg gaa aat ctt caa cga gaa gac ctg tct ccg ctt gaa gaa      869
Ala Leu Leu Glu Asn Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu
            110                 115                 120

gca aaa gcc tat gaa tct ttg ctc aaa cat ctc gat atg acc cag gaa      917
Ala Lys Ala Tyr Glu Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu
        125                 130                 135

cag ctg gcg aaa agg ctt gga aaa agc agg cct cac atc gcc aac cac      965
Gln Leu Ala Lys Arg Leu Gly Lys Ser Arg Pro His Ile Ala Asn His
140                 145                 150                 155

ttg cgg ctg ctg aca ctt cct gaa gac gtt caa aag tta atc gac aac     1013
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Leu Arg Leu Leu Thr Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn
                    160   165   170

ggc acg tta tcg atg ggc cat ggc cga aca ttg ctt gga ttg aaa aac   1061
Gly Thr Leu Ser Met Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn
                175   180   185

aag aaa aag ctt gag ccg ctt gtt caa aag gtc gtg tcc gaa cag ttg   1109
Lys Lys Lys Leu Glu Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu
            190   195   200

aac gtc cgc cag ttg gaa aag tta att caa cag ttg aac gct gat gtt   1157
Asn Val Arg Gln Leu Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val
        205   210   215

cca cgt gaa aca aag aag ccg aaa caa gtc aaa gat gca gtg atc aag   1205
Pro Arg Glu Thr Lys Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys
220   225   230   235

gaa cgg gaa tcg tat ttg cga aac tat ttt gga aca ccg gtg acc att   1253
Glu Arg Glu Ser Tyr Leu Arg Asn Tyr Phe Gly Thr Pro Val Thr Ile
                240   245   250

aaa aag caa aag aaa aaa ggc agg atc gaa atc gaa ttc tac tca aat   1301
Lys Lys Gln Lys Lys Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn
                255   260   265

gaa gac ttg gag cgt att ctc gaa tta ttg gct caa gaa gac gca   1346
Glu Asp Leu Glu Arg Ile Leu Glu Leu Leu Ala Gln Glu Asp Ala
            270   275   280

taagcttaaa aaccatctga tcatgtacag atggtttttt tatgacattc ttccggtcat   1406

tctttcaatt ggtgacacat ggcgccgctg cgatccggtc ttttccagat gcgacagccc   1466

gtccgcaagc acatttgcca tgctcatgac aagattgagc cttgtatttt gcaggacaaa   1526

atactccata aaaccgctga cattgacaat tccgttaata tgcacgtggc cgacttccgg   1586

caaacttttc tgaacgcctg ctcccggctt caaaggccct ttgccgattt ggaaagaccc   1646

cacgcttttg gttcgtccaa gacaggcgtc gatcgcgatc ataaaggat tttgatgctg   1706

ctgatgaata tgatcaagct tttcatttaa gttcacggcg tgaaccgggt cggcaagcgt   1766

tccatagaca tgaaaacgtg tcagctgctt tgcggagagt ttcattccta cgaggggacc   1826

                                                                       1849
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<211> 282

<212> PRT

<213> Bacillus licheniformis

<400> 47

Met Pro Lys Gly Leu Gly Lys Gly Ile Asn Ala Leu Phe Ser Asn Val
1   5   10   15

Asp Leu Ser Glu Glu Thr Val Glu Glu Ile Lys Leu Gln Asp Leu Arg
            20   25   30

Page 67

Pro Asn Pro Tyr Gln Pro Arg Lys Thr Phe Asp Asp Gln Ser Leu Lys
        35   40   45

Asp Leu Lys Glu Ser Ile Leu Gln His Gly Val Leu Gln Pro Ile Ile
    50   55   60

Val Arg Lys Ser Ile Lys Gly Tyr Asp Ile Val Ala Gly Glu Arg Arg
65   70   75   80

Phe Arg Ala Ala Glu Lys Ala Gly Leu Glu Thr Ile Pro Ala Ile Val
                85   90   95

Arg Glu Leu Ser Glu Ser Leu Met Met Glu Ile Ala Leu Leu Glu Asn
            100   105   110

Leu Gln Arg Glu Asp Leu Ser Pro Leu Glu Glu Ala Lys Ala Tyr Glu
        115   120   125

Ser Leu Leu Lys His Leu Asp Met Thr Gln Glu Gln Leu Ala Lys Arg
    130   135   140

Leu Gly Lys Ser Arg Pro His Ile Ala Asn His Leu Arg Leu Leu Thr
145   150   155   160

Leu Pro Glu Asp Val Gln Lys Leu Ile Asp Asn Gly Thr Leu Ser Met
                165   170   175

Gly His Gly Arg Thr Leu Leu Gly Leu Lys Asn Lys Lys Lys Leu Glu
            180   185   190

Pro Leu Val Gln Lys Val Val Ser Glu Gln Leu Asn Val Arg Gln Leu
        195   200   205

Glu Lys Leu Ile Gln Gln Leu Asn Ala Asp Val Pro Arg Glu Thr Lys
    210   215   220

Lys Pro Lys Gln Val Lys Asp Ala Val Ile Lys Glu Arg Glu Ser Tyr
225   230   235   240

Leu Arg Asn Tyr Phe Gly Thr Pro Val Thr Ile Lys Lys Gln Lys Lys
                245   250   255

Lys Gly Arg Ile Glu Ile Glu Phe Tyr Ser Asn Glu Asp Leu Glu Arg
            260   265   270

Ile Leu Glu Leu Leu Ala Gln Glu Asp Ala .
        275   280

<210>   48

<211> 3490

<212> DNA

<213> Bacillus licheniformis

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<222> (501)..(2987)

<223>

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agaaatcaac aacatggcgg tgtagctcag ctggctagag cgtacggttc atacccgtga     180

ggtcgggggt tcgatcccct ccgccgctac ttatatgaag gcccgttggt caagtggtta     240

agacaccgcc ctttcacggc ggtaacacgg gttcgaatcc cgtacgggtc attccggaaa     300

ccggcttctt ctgaagccgg ttttttgctg cataaaaata tgcaaaataa cgggaatgga     360

ctcgacttat caagagtgat tgaagcatgc tacaaaaagc gtcgaacagt tctttgaatt     420

cgttaccttc ttttgacaaa atcctatttc atctttcgct ataatggcaa gcaacgaata     480

aacgagtggg agatgagagc atg gaa aaa gcg gaa aga aga gtg aac agc cca      533
                        Met Glu Lys Ala Glu Arg Arg Val Asn Ser Pro
                        1               5                   10

ata gct gga cct gct gtt caa aaa ttg tat tca tgg ttt ggc agc atg      581
Ile Ala Gly Pro Ala Val Gln Lys Leu Tyr Ser Trp Phe Gly Ser Met
        15               20                   25

acg aag ctt atg atg cag cat tta tat tcc ctc ttt ttt tat aaa ggg      629
Thr Lys Leu Met Met Gln His Leu Tyr Ser Leu Phe Phe Tyr Lys Gly
        30               35                   40

ctg atc tat atg gtc atc ggt ttt tta ttg gga cga gcc ttc att ctg      677
Leu Ile Tyr Met Val Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu
    45               50                   55

tca gag gtc att ccc ttt gct ctt cca ttt ttc gga gcg atg ctt tta      725
Ser Glu Val Ile Pro Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu
60               65               70                   75

atc aaa aaa gat aaa gct ttc ctt gca tgc ctg gcg ctt ctt gcc gga      773
Ile Lys Lys Asp Lys Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly
                80               85                   90

gct ctg agc ata tcg cct cag cat tcg ctg ttc gtg ctt gcg gct ctg      821
Ala Leu Ser Ile Ser Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu
            95               100                  105

ttt gca ttt gcg ata tgt tca aaa atg acg tcc ctt att ata aaa gac      869
Phe Ala Phe Ala Ile Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp
            110              115                  120

cgt gtc aga acg ctg cct gtc gtc gtc ttt ttg gcg atg gct gtg aca      917
Arg Val Arg Thr Leu Pro Val Val Val Phe Leu Ala Met Ala Val Thr
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Arg Val Arg Thr Leu Pro Val Val Val Phe Leu Ala Met Ala Val Thr
125                 130             135

aga tgc gga ttc gta tat gcc gaa tac gga acg gtt tca ggt tat cac    965
Arg Cys Gly Phe Val Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His
140             145                 150                 155

tat att atg gct ttc gtt gaa gcc gga tta tcg ttt atc ctc aca ttg    1013
Tyr Ile Met Ala Phe Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu
                160             165                 170

att ttt ctg caa agc ctg ccg att gtc aca tca aag cgg gcg aaa cag    1061
Ile Phe Leu Gln Ser Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln
                175             180                 185

tcg ctg aaa att gaa gag atc att tgt ttt atg att tta atc gct tcc    1109
Ser Leu Lys Ile Glu Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser
            190             195                 200

gtt ctc acg ggc ttg aca ggc gtt tca ttt caa ggc atg cag gct gaa    1157
Val Leu Thr Gly Leu Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu
        205             210                 215

ctg ata ttg gcc cgt tat gtc gtg ctc gct ttc gcg ttc atc gga ggc    1205
Leu Ile Leu Ala Arg Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly
220             225                 230                 235

gca agc atc ggc tgt aca gtc ggg gtt gtg acc ggg ctg att ctc agc    1253
Ala Ser Ile Gly Cys Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser
                240             245                 250

ctc tca aac atc ggc aat tta tat cag atg agc ctg ctg gct ttc tca    1301
Leu Ser Asn Ile Gly Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser
                255             260                 265

ggc ctt ctc ggc ggt ttg cta aaa gaa gga aaa aag ttc ggc gca gcg    1349
Gly Leu Leu Gly Gly Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala
                270             275                 280

gtc ggc tta ttg att gga tct cta ttg att tct ctg tac gga gaa ggt    1397
Val Gly Leu Leu Ile Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly
285                 290                 295

tcg gct gaa tta gtg ccg acg ctt tat gaa tct ctg att gca atc ggc    1445
Ser Ala Glu Leu Val Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly
300                 305                 310                 315

ctg ttc ctt tta acc cct cag tcg att acg aaa aaa gtg gcc aag tat    1493
Leu Phe Leu Leu Thr Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr
                320             325                 330

ata cct gga acg act gag cac gcc cag gaa cag cag cag tat gca agg    1541
Ile Pro Gly Thr Thr Glu His Ala Gln Glu Gln Gln Gln Tyr Ala Arg
                335             340                 345

aaa atc cgc gat gtc acc gcc caa aaa gtc gat cag ttt tcg aac gtt    1589
Lys Ile Arg Asp Val Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val
                350             355                 360

ttt cac gct tta tcc gaa agc ttc gct acc ttt tat cat tca gct ccg    1637
Phe His Ala Leu Ser Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro
                365             370                 375

gac gat gaa gga aaa gaa aaa gag atc gat ctg ttt ttg agc acg gtg    1685
Asp Asp Glu Gly Lys Glu Lys Glu Ile Asp Leu Phe Leu Ser Thr Val
380                 385                 390                 395

aca gaa cat tcc tgt cag tca tgc tat aag aaa aac aag tgc tgg gtt    1733
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Page 70

Thr Glu His Ser Cys Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val
              400   405   410

cag aac ttt gat aaa aca tat gat ttg atg aaa cgg gtt atg cag gaa   1781
Gln Asn Phe Asp Lys Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu
              415   420   425

acg gaa gaa aag caa tat ttt aaa aac cgc aag ctg aaa aag gag ttt   1829
Thr Glu Glu Lys Gln Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe
              430   435   440

cat cag cac tgc tcc aaa tca aag caa gta gaa gcg ctg att gaa gac   1877
His Gln His Cys Ser Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp
              445   450   455

gag ctg act cat ttt agg gcg aac cag aca tta aaa caa aag gtg cat   1925
Glu Leu Thr His Phe Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His
460   465   470   475

gac agc aga cgt ctc gtt gca gag cag ctt ctc ggc gtt tct cag gtt   1973
Asp Ser Arg Arg Leu Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val
              480   485   490

atg gcg gac ttt tct cgg gaa ata aaa agg gaa agg gag cag cat ttt   2021
Met Ala Asp Phe Ser Arg Glu Ile Lys Arg Glu Arg Glu Gln His Phe
              495   500   505

att caa gaa gag caa att cgg gat gcg ctg cag cac ttc ggc atc gag   2069
Ile Gln Glu Glu Gln Ile Arg Asp Ala Leu Gln His Phe Gly Ile Glu
              510   515   520

att cag caa gtc gaa ata tac agc ctt gag cag gga aac atc gat att   2117
Ile Gln Gln Val Glu Ile Tyr Ser Leu Glu Gln Gly Asn Ile Asp Ile
              525   530   535

gaa atg agt atc ccg tat tgc aac ggc cat gga gag tgt gaa aaa atc   2165
Glu Met Ser Ile Pro Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile
540   545   550   555

atc gct ccg atg ctg tcc gat att ttg gaa gaa caa att atc gtc aaa   2213
Ile Ala Pro Met Leu Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys
              560   565   570

gca gaa cag tgc gcc ggc cat ccg aat gga tat tgt cat gtt gcc ttc   2261
Ala Glu Gln Cys Ala Gly His Pro Asn Gly Tyr Cys His Val Ala Phe
              575   580   585

ggt tcg gcg aag tca tac agg gtg gtg aca gga gcc gcg cat gca gca   2309
Gly Ser Ala Lys Ser Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala
              590   595   600

aaa ggc gga ggg ctt gtc tcc ggc gac agc tac aat atg atg gag ctc   2357
Lys Gly Gly Gly Leu Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu
              605   610   615

ggc acc ggc aaa tat gcc gcc gcc att agc gat ggt atg gga aat ggc   2405
Gly Thr Gly Lys Tyr Ala Ala Ala Ile Ser Asp Gly Met Gly Asn Gly
620   625   630   635

gca agg gcc cat ttt gaa agc aat gag acg atc aag ctg ctg gaa aag   2453
Ala Arg Ala His Phe Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys
              640   645   650

att ctt cag tcg ggc atc gac gaa aaa gtg gcg att aaa acg att aac   2501
Ile Leu Gln Ser Gly Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn
              655   660   665

agc att ctt tca tta agg aca aca gat gaa att tat tcg aca ttg gat   2549
Page 71

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Ser Ile Leu Ser Leu Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp
        670             675                 680

tta tcg gtc atc gat ctt cag gat gcg agc tgc aag ttt ttg aaa atc    2597
Leu Ser Val Ile Asp Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile
        685             690                 695

ggc tcc acc ccg agc ttt att aaa aga ggc gat caa att ata aaa gtg    2645
Gly Ser Thr Pro Ser Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val
700             705                 710                 715

cag gcc agc aat ctg ccg atc ggc atc att aca gaa ttc gat gtc gat    2693
Gln Ala Ser Asn Leu Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp
                720                 725                 730

gtt gtc agc gag caa tta aaa gcg gga gac ctt ttg atc atg atg agc    2741
Val Val Ser Glu Gln Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser
                735                 740                 745

gac gga atc ttt gaa ggg ccg aga cat gtg gaa aat cat gat ctg tgg    2789
Asp Gly Ile Phe Glu Gly Pro Arg His Val Glu Asn His Asp Leu Trp
            750                 755                 760

atg aag cgc aaa ttg aaa tcg ctg aaa acc gag gag ccg cag gaa atc    2837
Met Lys Arg Lys Leu Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile
        765             770                 775

gcc gac tta atc atg gaa gaa gtg atc cgg aca agg tcg ggt ctg att    2885
Ala Asp Leu Ile Met Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile
780             785                 790                 795

gag gac gac atg acg gtg att gtc atc aag ctg gac cat aat acg cca    2933
Glu Asp Asp Met Thr Val Ile Val Ile Lys Leu Asp His Asn Thr Pro
                800                 805                 810

aag tgg gcc tcc att ccg gcg ccg gct ttt ttc caa aag aat caa gag    2981
Lys Trp Ala Ser Ile Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu
                815                 820                 825

att tct tagcattcgt ataaatcaaa tttcttctgg cgatgatgga actaaatcaa    3037
Ile Ser

gatatctttg tccaggagga ataaaaacga tgaaaaaggg gcatttgaat caaatcctgc    3097

ttttgacgga cggctgttca aaccgcggcg aagacccgca ggccatggct gcctttgcga    3157

aagagcaggg aattaccgtg aatgtgattg ggattatgga cgagcatgaa atggatcagg    3217

aggcgatgaa agaagtcgaa gggatcgctc tcgcaggcgg aggagttcac caggtggttt    3277

acacgtcgca gctgtcgcag accgttcaaa tggtgacaaa aaaggcgatg acgcaaaccc    3337

ttcaaggcgt ggtcaacagt gagctcaaac aaattctcgg caagcatacc gaaatggatg    3397

aactgcctcc tgataaacgc ggtgaagtca tggaagtcgt tgacgagctt ggtgagaccg    3457

tgcatcttca tgtactggtt cttgtcgata caa                                3490
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<210>   49

<211>   829

<212>   PRT

<213>   Bacillus licheniformis

Page 72

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1   5   10   15

Val Gln Lys Leu Tyr Ser Trp Phe Gly Ser Met Thr Lys Leu Met Met
            20   25   30

Gln His Leu Tyr Ser Leu Phe Phe Tyr Lys Gly Leu Ile Tyr Met Val
        35   40   45

Ile Gly Phe Leu Leu Gly Arg Ala Phe Ile Leu Ser Glu Val Ile Pro
    50   55   60

Phe Ala Leu Pro Phe Phe Gly Ala Met Leu Leu Ile Lys Lys Asp Lys
65   70   75   80

Ala Phe Leu Ala Cys Leu Ala Leu Leu Ala Gly Ala Leu Ser Ile Ser
                85   90   95

Pro Gln His Ser Leu Phe Val Leu Ala Ala Leu Phe Ala Phe Ala Ile
            100   105   110

Cys Ser Lys Met Thr Ser Leu Ile Ile Lys Asp Arg Val Arg Thr Leu
            115   120   125

Pro Val Val Val Phe Leu Ala Met Ala Val Thr Arg Cys Gly Phe Val
    130   135   140

Tyr Ala Glu Tyr Gly Thr Val Ser Gly Tyr His Tyr Ile Met Ala Phe
145   150   155   160

Val Glu Ala Gly Leu Ser Phe Ile Leu Thr Leu Ile Phe Leu Gln Ser
                165   170   175

Leu Pro Ile Val Thr Ser Lys Arg Ala Lys Gln Ser Leu Lys Ile Glu
            180   185   190

Glu Ile Ile Cys Phe Met Ile Leu Ile Ala Ser Val Leu Thr Gly Leu
        195   200   205

Thr Gly Val Ser Phe Gln Gly Met Gln Ala Glu Leu Ile Leu Ala Arg
    210   215   220

Tyr Val Val Leu Ala Phe Ala Phe Ile Gly Gly Ala Ser Ile Gly Cys
225   230   235   240

Thr Val Gly Val Val Thr Gly Leu Ile Leu Ser Leu Ser Asn Ile Gly
            245   250   255

Asn Leu Tyr Gln Met Ser Leu Leu Ala Phe Ser Gly Leu Leu Gly Gly
        260   265   270

Leu Leu Lys Glu Gly Lys Lys Phe Gly Ala Ala Val Gly Leu Leu Ile
        275   280   285

Gly Ser Leu Leu Ile Ser Leu Tyr Gly Glu Gly Ser Ala Glu Leu Val
    290   295   300

Pro Thr Leu Tyr Glu Ser Leu Ile Ala Ile Gly Leu Phe Leu Leu Thr
305   310   315   320

Pro Gln Ser Ile Thr Lys Lys Val Ala Lys Tyr Ile Pro Gly Thr Thr
            325   330   335

Glu His Ala Gln Glu Gln Gln Gln Tyr Ala Arg Lys Ile Arg Asp Val
            340   345   350

Thr Ala Gln Lys Val Asp Gln Phe Ser Asn Val Phe His Ala Leu Ser
        355   360   365

Glu Ser Phe Ala Thr Phe Tyr His Ser Ala Pro Asp Asp Glu Gly Lys
    370   375   380

Glu Lys Glu Ile Asp Leu Phe Leu Ser Thr Val Thr Glu His Ser Cys
385   390   395   400

Gln Ser Cys Tyr Lys Lys Asn Lys Cys Trp Val Gln Asn Phe Asp Lys
            405   410   415

Thr Tyr Asp Leu Met Lys Arg Val Met Gln Glu Thr Glu Glu Lys Gln
            420   425   430

Tyr Phe Lys Asn Arg Lys Leu Lys Lys Glu Phe His Gln His Cys Ser
        435   440   445

Lys Ser Lys Gln Val Glu Ala Leu Ile Glu Asp Glu Leu Thr His Phe
    450   455   460

Arg Ala Asn Gln Thr Leu Lys Gln Lys Val His Asp Ser Arg Arg Leu
465   470   475   480

Val Ala Glu Gln Leu Leu Gly Val Ser Gln Val Met Ala Asp Phe Ser
            485   490   495

Arg Glu Ile Lys Arg Glu Arg Glu Gln His Phe Ile Gln Glu Glu Gln
            500   505   510

Ile Arg Asp Ala Leu Gln His Phe Gly Ile Glu Ile Gln Gln Val Glu
        515   520   525

Page 74

Ile Tyr Ser Leu Glu Gln Gly Asn Ile Asp Ile Glu Met Ser Ile Pro
    530   535   540

Tyr Cys Asn Gly His Gly Glu Cys Glu Lys Ile Ile Ala Pro Met Leu
545   550   555   560

Ser Asp Ile Leu Glu Glu Gln Ile Ile Val Lys Ala Glu Gln Cys Ala
                565   570   575

Gly His Pro Asn Gly Tyr Cys His Val Ala Phe Gly Ser Ala Lys Ser
            580   585   590

Tyr Arg Val Val Thr Gly Ala Ala His Ala Ala Lys Gly Gly Gly Leu
        595   600   605

Val Ser Gly Asp Ser Tyr Asn Met Met Glu Leu Gly Thr Gly Lys Tyr
    610   615   620

Ala Ala Ala Ile Ser Asp Gly Met Gly Asn Gly Ala Arg Ala His Phe
625   630   635   640

Glu Ser Asn Glu Thr Ile Lys Leu Leu Glu Lys Ile Leu Gln Ser Gly
            645   650   655

Ile Asp Glu Lys Val Ala Ile Lys Thr Ile Asn Ser Ile Leu Ser Leu
            660   665   670

Arg Thr Thr Asp Glu Ile Tyr Ser Thr Leu Asp Leu Ser Val Ile Asp
        675   680   685

Leu Gln Asp Ala Ser Cys Lys Phe Leu Lys Ile Gly Ser Thr Pro Ser
    690   695   700

Phe Ile Lys Arg Gly Asp Gln Ile Ile Lys Val Gln Ala Ser Asn Leu
705   710   715   720

Pro Ile Gly Ile Ile Thr Glu Phe Asp Val Asp Val Val Ser Glu Gln
            725   730   735

Leu Lys Ala Gly Asp Leu Leu Ile Met Met Ser Asp Gly Ile Phe Glu
            740   745   750

Gly Pro Arg His Val Glu Asn His Asp Leu Trp Met Lys Arg Lys Leu
            755   760   765

Lys Ser Leu Lys Thr Glu Glu Pro Gln Glu Ile Ala Asp Leu Ile Met
    770   775   780

Glu Glu Val Ile Arg Thr Arg Ser Gly Leu Ile Glu Asp Asp Met Thr
785   790   795   800

Page 75

Val Ile Val Ile Lys Leu Asp His Asn Thr Pro Lys Trp Ala Ser Ile
         805   810   815

Pro Ala Pro Ala Phe Phe Gln Lys Asn Gln Glu Ile Ser
        820   825

<210> 50

<211> 1928

<212> DNA

<213> Bacillus licheniformis

<220>

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<222> (501)..(1427)

<223>

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ttcaaaaccg ctgcccaaaa cgtaacggag ctgccgatca gagaagtctc aaaaggaaaa      180

tatgaaggat attggaccgc tacttcaact gcaaaagcaa aaggagcgga aatcgaggtc      240

atcgtcagag atgattacgg caatgaaacg agacaaacgg caaaaggcaa gctgtatatc      300

aatgaaaagc tgaaataaag gtgaaaagac gctgtcttta atggcagcgt ttttttcgtt      360

ttacgatcga caaattcagt acgaaaactt caaaaaatgt acgatttacg caacattaat      420

tgacagactt tacctttggg cttgatttat acttaggaaa acaaacacta aggtcaccga      480

gccgcagaaa ggggaaggat gtg gaa atc tat tta gat gcg ata tgg ctg tta      533
                        Val Glu Ile Tyr Leu Asp Ala Ile Trp Leu Leu
                         1               5                  10

aac ttt tgt ttt gac ttg ctg ctt tta atg atg acc gca ttt att tta      581
Asn Phe Cys Phe Asp Leu Leu Leu Leu Met Met Thr Ala Phe Ile Leu
             15               20               25

aag cga agg gtt aaa aag cgg agg ctg atc cta ggg gca ttt gtc gcg      629
Lys Arg Arg Val Lys Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala
         30               35               40

tca agc atc gtt ctg ttt atg ttt aca cct ttt tca ccg tac gtc ctt      677
Ser Ser Ile Val Leu Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu
     45               50               55

cat cct gcc ggc aaa ctg tcg ttt tcg gtt gtg atc gtt ctt gtg gca      725
His Pro Ala Gly Lys Leu Ser Phe Ser Val Val Ile Val Leu Val Ala
60               65               70               75

ttt ggt ttt aag cgg ttc cgg ttt ttt ttg cag aat ttg ttt tct ttt      773
Phe Gly Phe Lys Arg Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe
             80               85               90
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tat ttt gcc act ttt tta atg gga gga ggg att atc gga gcg cat tct    821
Tyr Phe Ala Thr Phe Leu Met Gly Gly Gly Ile Ile Gly Ala His Ser
            95                  100                 105

ttg ctt gaa acg gat tcg atc atg gaa aac ggc gtc ttt atg acg aat    869
Leu Leu Glu Thr Asp Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn
            110                 115                 120

tgg tcc ggt ttt gga gac ccc gtc agc tgg ctg ttt gtc tgt gtg ggt    917
Trp Ser Gly Phe Gly Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly
    125                 130                 135

ttt gcg gct gta tgg ctg ttt tca aaa aag cgt ttt gaa gat gct gaa    965
Phe Ala Ala Val Trp Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu
140                 145                 150                 155

gcg aag aaa att caa tac gaa gaa cgc gtc cgc cta gag gcc tgc att    1013
Ala Lys Lys Ile Gln Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile
                160                 165                 170

ggt gaa cat acg ctt cat ttc acc gga ttg att gac tcc gga aac cag    1061
Gly Glu His Thr Leu His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln
                175                 180                 185

ctc tac gat cca atc aca aaa acg ccc gtc atg atc gtc aat att gaa    1109
Leu Tyr Asp Pro Ile Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu
            190                 195                 200

aaa ttg aaa gtt gta ttg gga gaa gag gca agt gtg acc atc aag gaa    1157
Lys Leu Lys Val Val Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu
205                 210                 215

atg agc ccg ctt gat gcc gtc ggg aaa ctg gat gaa gca ctg ccg tat    1205
Met Ser Pro Leu Asp Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr
220                 225                 230                 235

atc ggg cgg atc cgc ctg att ccg tac cgc ggg gtc ggc cat cag cat    1253
Ile Gly Arg Ile Arg Leu Ile Pro Tyr Arg Gly Val Gly His Gln His
                240                 245                 250

cag ttt ctg ctc tgc tta aag ccg gat cat gtg ctc gtt tgt acg gaa    1301
Gln Phe Leu Leu Cys Leu Lys Pro Asp His Val Leu Val Cys Thr Glu
                255                 260                 265

aga gaa gtg att gaa gcg ccg aaa tgc ctg att ggc atc agc aca tca    1349
Arg Glu Val Ile Glu Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser
            270                 275                 280

ccg ctt tcc gct gac ggc gaa ttt gac gcc atc gtc cat ccg aaa atg    1397
Pro Leu Ser Ala Asp Gly Glu Phe Asp Ala Ile Val His Pro Lys Met
285                 290                 295

ctg gcc gga aac ccg gtc aaa cac gtt tct taaacttgaa gtctgttaca       1447
Leu Ala Gly Asn Pro Val Lys His Val Ser
300                 305

ttatcatact cctgaagacg tttatttaga aggggagga agatgaaaaa actaaaatta   1507

aggttaacct atctatggta caaacttta atgaaactgg ggctgaaaag cgacgaaatt    1567

tattatatcg gcggaagcga ggcgcttccc ccgccattgt caaaagatga agagcaggtg   1627

cttctccata agctgcctga cggtgatcag gcggcacgag cgattttgat tgaacgaaat   1687

ctcagactgg tcgtgtacat cgcgagaaaa tttgaaaata caggaatcaa tatcgaggat   1747

ttaatctcca tcggcacgat cgggctcatc aaagcggtga atacgtttaa tcccgagaaa   1807
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Page 77

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aaaatcaaac tggctacata tgcttccaga tgcattgaaa atgaaatttt gatgtattta    1867
agaagaaaca ataaaatccg ttcagaggta tcattcgacg aaccgctgaa catcgattgg    1927
g                                                                     1928
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<210>   51

<211>   309

<212>   PRT

<213>   Bacillus licheniformis

<400>   51

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1               5                   10                  15

Leu Leu Leu Leu Met Met Thr Ala Phe Ile Leu Lys Arg Arg Val Lys
            20                  25                  30

Lys Arg Arg Leu Ile Leu Gly Ala Phe Val Ala Ser Ser Ile Val Leu
        35                  40                  45

Phe Met Phe Thr Pro Phe Ser Pro Tyr Val Leu His Pro Ala Gly Lys
    50                  55                  60

Leu Ser Phe Ser Val Val Ile Val Leu Val Ala Phe Gly Phe Lys Arg
65                  70                  75                  80

Phe Arg Phe Phe Leu Gln Asn Leu Phe Ser Phe Tyr Phe Ala Thr Phe
                85                  90                  95

Leu Met Gly Gly Gly Ile Ile Gly Ala His Ser Leu Leu Glu Thr Asp
                100                 105                 110

Ser Ile Met Glu Asn Gly Val Phe Met Thr Asn Trp Ser Gly Phe Gly
            115                 120                 125

Asp Pro Val Ser Trp Leu Phe Val Cys Val Gly Phe Ala Ala Val Trp
    130                 135                 140

Leu Phe Ser Lys Lys Arg Phe Glu Asp Ala Glu Ala Lys Lys Ile Gln
145                 150                 155                 160

Tyr Glu Glu Arg Val Arg Leu Glu Ala Cys Ile Gly Glu His Thr Leu
                165                 170                 175

His Phe Thr Gly Leu Ile Asp Ser Gly Asn Gln Leu Tyr Asp Pro Ile
                180                 185                 190
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Thr Lys Thr Pro Val Met Ile Val Asn Ile Glu Lys Leu Lys Val Val
        195             200             205

Leu Gly Glu Glu Ala Ser Val Thr Ile Lys Glu Met Ser Pro Leu Asp
    210             215             220

Ala Val Gly Lys Leu Asp Glu Ala Leu Pro Tyr Ile Gly Arg Ile Arg
225             230             235             240

Leu Ile Pro Tyr Arg Gly Val Gly His Gln His Gln Phe Leu Leu Cys
            245             250             255

Leu Lys Pro Asp His Val Leu Val Cys Thr Glu Arg Glu Val Ile Glu
        260             265             270

Ala Pro Lys Cys Leu Ile Gly Ile Ser Thr Ser Pro Leu Ser Ala Asp
        275             280             285

Gly Glu Phe Asp Ala Ile Val His Pro Lys Met Leu Ala Gly Asn Pro
290             295             300

Val Lys His Val Ser
305
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<210> 52

<211> 1922

<212> DNA

<213> Bacillus licheniformis

<220>

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<222> (501)..(1421)

<223>

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taagatcatg aagctttttct ttggacaagt caatccgacg gttttgacaa tggcggcgtt   180
aagggtggta tcatctttga tcgaactgac ggcggctgtt gtgatgcttt tgacaaacga   240
cgtcagaaaa gctgtggcgg tcaacagcgt actggccatg gtcgggccgc tcatctttat   300
tattacaatg acaatcggca tctatcagat tgcagggcag ctttcttacg caaagctgat   360
tttgatcttt atgggagtgg ttttgatcat cgcggggatc tataaatagc gacacatgat   420
aagagaggcc gacttgtcat aatgtcttcc tttgatcata cattttttata gaagacaagc   480
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aaaaagagga gggagtgttt ttg cac cac atc aca gag att ctc ccc gat acg     533
                      Leu His His Ile Thr Glu Ile Leu Pro Asp Thr
                       1                 5                 10

atc aaa cgc gcg ctc agc ggt ctt ggc gac cat gaa atc gat cag ata     581
Ile Lys Arg Ala Leu Ser Gly Leu Gly Asp His Glu Ile Asp Gln Ile
            15              20                  25

gaa gaa att cgg gtt cgg aca agt cgt ccg ctg gaa ctg gtg aac aaa     629
Glu Glu Ile Arg Val Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys
        30                  35                  40

gga aag ccg cgc ttt ctc cct tat gtg gcg acg cct gaa gac tcg gcg     677
Gly Lys Pro Arg Phe Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala
    45                  50                  55

ctt ctt tta aac aga ttg gga aat tac agc atg tat aca ctg gaa gag     725
Leu Leu Leu Asn Arg Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu
60                  65                  70                  75

gaa ttg aaa aaa gga tat gtc acg atc aga ggc gga cac cgc gtg ggg     773
Glu Leu Lys Lys Gly Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly
                80                  85                  90

ctt gcc ggc cgg gtt gtc gtc gaa aac ggg gcc gtc aaa gga atc aga     821
Leu Ala Gly Arg Val Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg
                95                  100                 105

gaa ata tca tca ttt aat att cgc att gcc aaa gaa aaa atc ggc att     869
Glu Ile Ser Ser Phe Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile
        110                 115                 120

tcc aaa ccg tat gtc ccc cat tta ttt caa aac tcg tgg ctg aac acg     917
Ser Lys Pro Tyr Val Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr
    125                 130                 135

ctg att atc ggt ccg ccg caa acc gga aaa aca aca ctg ctc aga gac    ·965
Leu Ile Ile Gly Pro Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp
140                 145                 150                 155

ctc gcc agg ctg atc agt tcg gga agc ggc aac gcc cct gcc aaa aaa     1013
Leu Ala Arg Leu Ile Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys
                160                 165                 170

gtg ggg att gtt gac gaa agg tct gaa atc gca ggc tgt gta aac ggc     1061
Val Gly Ile Val Asp Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly
                175                 180                 185

ata ccg caa tat cgg ctc ggc gac cgg gca gac atc ctt gac gcc tgt     1109
Ile Pro Gln Tyr Arg Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys
            190                 195                 200

cca aaa gcg gaa ggg ctg atg atg atg atc aga tcg atg agt ccg gag     1157
Pro Lys Ala Glu Gly Leu Met Met Met Ile Arg Ser Met Ser Pro Glu
    205                 210                 215

gta atg atc gcc gat gag atc ggg aga atg gaa gac gca gaa gcg ctc     1205
Val Met Ile Ala Asp Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu
220                 225                 230                 235

ttg gaa gcg gtc cac gcg ggg gtg act gtc atc gtt tcg gct cac ggc     1253
Leu Glu Ala Val His Ala Gly Val Thr Val Ile Val Ser Ala His Gly
                240                 245                 250

tac aca tat gca gat ctc gcc agg cgt cca tca ttg aaa atg ctt caa     1301
Tyr Thr Tyr Ala Asp Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln
                255                 260                 265
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gag cac cgg gtt ttt gag cga atc gtg gaa ctt tcc aga aag aac ggt      1349
Glu His Arg Val Phe Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly
        270             275             280

ccc ggc agc ctg agc cgc atc cta aat ggg aac gga gag ccg ctc ggg      1397
Pro Gly Ser Leu Ser Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly
        285             290             295

gca gca aag agg atg tta tca tgc tgaagctttt aggtgccgtg cttattttgg     1451
Ala Ala Lys Arg Met Leu Ser Cys
300             305

cagcagccac atggacagga tttgaaatgg cgaagccttt cagggaaagg ccgaagcaaa    1511

tccgccagct gttggccgct ttgcagtctt tggaggctga aatcatgtac gggcatacac    1571

cgctccgtca ggcatcaaaa cagatcgcac accagcttac cgagccggta gcctctttgt    1631

ttcagacatt tgcagaacag cttgaaaaag gcagcgcttc agcagggacg gcatgggaag    1691

acagcctgga gaaagtatgg cccgaaacgg ctcttaaaaa gaaagaatac gagattttac    1751

ggcaattcgg cgaaacgctg gccgtcatg atctgatttc tcagcaaaaa catatcaaac     1811

tggcgttaac ccatttagag acagaggaag ctgaagcaaa tctcgcccag gcgaaaaatg    1871

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<211> 307

<212> PRT

<213> Bacillus licheniformis

<400> 53

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            20              25              30

Arg Thr Ser Arg Pro Leu Glu Leu Val Asn Lys Gly Lys Pro Arg Phe
        35              40              45

Leu Pro Tyr Val Ala Thr Pro Glu Asp Ser Ala Leu Leu Leu Asn Arg
    50              55              60

Leu Gly Asn Tyr Ser Met Tyr Thr Leu Glu Glu Glu Leu Lys Lys Gly
65              70              75              80

Tyr Val Thr Ile Arg Gly Gly His Arg Val Gly Leu Ala Gly Arg Val
                85              90              95

Val Val Glu Asn Gly Ala Val Lys Gly Ile Arg Glu Ile Ser Ser Phe
            100             105             110
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Asn Ile Arg Ile Ala Lys Glu Lys Ile Gly Ile Ser Lys Pro Tyr Val
        115   120   125

Pro His Leu Phe Gln Asn Ser Trp Leu Asn Thr Leu Ile Ile Gly Pro
    130   135   140

Pro Gln Thr Gly Lys Thr Thr Leu Leu Arg Asp Leu Ala Arg Leu Ile
145   150   155   160

Ser Ser Gly Ser Gly Asn Ala Pro Ala Lys Lys Val Gly Ile Val Asp
                165   170   175

Glu Arg Ser Glu Ile Ala Gly Cys Val Asn Gly Ile Pro Gln Tyr Arg
            180   185   190

Leu Gly Asp Arg Ala Asp Ile Leu Asp Ala Cys Pro Lys Ala Glu Gly
        195   200   205

Leu Met Met Met Ile Arg Ser Met Ser Pro Glu Val Met Ile Ala Asp
    210   215   220

Glu Ile Gly Arg Met Glu Asp Ala Glu Ala Leu Leu Glu Ala Val His
225   230   235   240

Ala Gly Val Thr Val Ile Val Ser Ala His Gly Tyr Thr Tyr Ala Asp
                245   250   255

Leu Ala Arg Arg Pro Ser Leu Lys Met Leu Gln Glu His Arg Val Phe
            260   265   270

Glu Arg Ile Val Glu Leu Ser Arg Lys Asn Gly Pro Gly Ser Leu Ser
        275   280   285

Arg Ile Leu Asn Gly Asn Gly Glu Pro Leu Gly Ala Ala Lys Arg Met
    290   295   300

Leu Ser Cys
305

<210>   54

<211>   1511

<212>   DNA

<213>   Bacillus licheniformis

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<222>   (498)..(1010)

<223>

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<222>   (1036)..(1239)

<223>

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<221>   CDS

<222>   (1255)..(1509)

<223>

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atcgcaggct gtgtaaacgg cataccgcaa tatcggctcg gcgaccgggc agacatcctt    180

gacgcctgtc caaaagcgga agggctgatg atgatgatca gatcgatgag tccggaggta    240

atgatcgccg atgagatcgg gagaatggaa gacgcagaag cgctcttgga agcggtccac    300

gcgggggtga ctgtcatcgt ttcggctcac ggctacacat atgcagatct cgccaggcgt    360

ccatcattga aaatgcttca gagcaccgg gttttgagc gaatcgtgga actttccaga    420

aagaacggtc ccggcagcct gagccgcatc ctaaatggga acggagagcc gctcggggca    480

gcaaagagga tgttatc atg ctg aag ctt tta ggt gcc gtg ctt att ttg       530
                    Met Leu Lys Leu Leu Gly Ala Val Leu Ile Leu
                    1           5                   10

gca gca gcc aca tgg aca gga ttt gaa atg gcg aag cct ttc agg gaa      578
Ala Ala Ala Thr Trp Thr Gly Phe Glu Met Ala Lys Pro Phe Arg Glu
            15                  20                  25

agg ccg aag caa atc cgc cag ctg ttg gcc gct ttg cag tct ttg gag      626
Arg Pro Lys Gln Ile Arg Gln Leu Leu Ala Ala Leu Gln Ser Leu Glu
        30                  35                  40

gct gaa atc atg tac ggg cat aca ccg ctc cgt cag gca tca aaa cag      674
Ala Glu Ile Met Tyr Gly His Thr Pro Leu Arg Gln Ala Ser Lys Gln
    45                  50                  55

atc gca cac cag ctt acc gag ccg gta gcc tct ttg ttt cag aca ttt      722
Ile Ala His Gln Leu Thr Glu Pro Val Ala Ser Leu Phe Gln Thr Phe
60                  65                  70                  75

gca gaa cag ctt gaa aaa ggc agc gct tca gca ggg acg gca tgg gaa      770
Ala Glu Gln Leu Glu Lys Gly Ser Ala Ser Ala Gly Thr Ala Trp Glu
                80                  85                  90

gac agc ctg gag aaa gta tgg ccc gaa acg gct ctt aaa aag aaa gaa      818
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Page 83

Asp Ser Leu Glu Lys Val Trp Pro Glu Thr Ala Leu Lys Lys Lys Glu
          95   100   105

tac gag att tta cgg caa ttc ggc gaa acg ctg ggc cgt cat gat ctg   866
Tyr Glu Ile Leu Arg Gln Phe Gly Glu Thr Leu Gly Arg His Asp Leu
          110   115   120

att tct cag caa aaa cat atc aaa ctg gcg tta acc cat tta gag aca   914
Ile Ser Gln Gln Lys His Ile Lys Leu Ala Leu Thr His Leu Glu Thr
125   130   135

gag gaa gct gaa gca aat ctc gcc cag gcg aaa aat gaa aaa atg gtc   962
Glu Glu Ala Glu Ala Asn Leu Ala Gln Ala Lys Asn Glu Lys Met Val
140   145   150   155

aaa agc ctt gga ttt ttg acg gga ctg cta ctg att ctt cta ttg atg   1010
Lys Ser Leu Gly Phe Leu Thr Gly Leu Leu Leu Ile Leu Leu Leu Met
              160   165   170

taatgaagag gggagcatac acgaa atg gga gta gac gta aat att att ttt   1062
                          Met Gly Val Asp Val Asn Ile Ile Phe
                                        175   180

caa att gcc ggc gtc ggg atc gtc gtc gct ttt ctt cac acc ata ctg   1110
Gln Ile Ala Gly Val Gly Ile Val Val Ala Phe Leu His Thr Ile Leu
              185   190   195

gat caa atg ggg aag aag gaa tat gcc caa tgg gtc acg ctt tta gga   1158
Asp Gln Met Gly Lys Lys Glu Tyr Ala Gln Trp Val Thr Leu Leu Gly
              200   205   210

ttc att tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc   1206
Phe Ile Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe
          215   220   225

caa aag ata aaa gct gtc ttt cta ttt caa gga tagggggct cactc att   1257
Gln Lys Ile Lys Ala Val Phe Leu Phe Gln Gly   Ile
          230   235   240

gaa atc gtt caa atc gta gga ctg gga atg atc gcc acc ttc ctc agc   1305
Glu Ile Val Gln Ile Val Gly Leu Gly Met Ile Ala Thr Phe Leu Ser
              245   250   255

ttg att gtg aaa gag caa aaa ccg acg ttt gct ttt ttg att gtc gtt   1353
Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val Val
              260   265   270

ttt gcc ggc tgc acg att ttt tta ttc tta gta gat cag gtc tac gaa   1401
Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr Glu
          275   280   285

atc att cgg atg att gaa aaa ata gct gcc aat gcc aac atc aac atg   1449
Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn Met
290   295   300

atg tat gtc gaa acg att ttg aag att atc ggg att gct tat att gcg   1497
Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile Ala
305   310   315   320

gag ttt ggc gcc ca   1511
Glu Phe Gly Ala

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<213> Bacillus licheniformis

<400> 55

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Thr Gly Phe Glu Met Ala Lys Pro Phe Arg Glu Arg Pro Lys Gln Ile
            20   25   30

Arg Gln Leu Leu Ala Ala Leu Gln Ser Leu Glu Ala Glu Ile Met Tyr
        35   40   45

Gly His Thr Pro Leu Arg Gln Ala Ser Lys Gln Ile Ala His Gln Leu
    50   55   60

Thr Glu Pro Val Ala Ser Leu Phe Gln Thr Phe Ala Glu Gln Leu Glu
65   70   75   80

Lys Gly Ser Ala Ser Ala Gly Thr Ala Trp Glu Asp Ser Leu Glu Lys
                85   90   95

Val Trp Pro Glu Thr Ala Leu Lys Lys Lys Glu Tyr Glu Ile Leu Arg
            100   105   110

Gln Phe Gly Glu Thr Leu Gly Arg His Asp Leu Ile Ser Gln Gln Lys
        115   120   125

His Ile Lys Leu Ala Leu Thr His Leu Glu Thr Glu Glu Ala Glu Ala
    130   135   .140

Asn Leu Ala Gln Ala Lys Asn Glu Lys Met Val Lys Ser Leu Gly Phe
145   150   155   160

Leu Thr Gly Leu Leu Leu Ile Leu Leu Leu Met
                165   170

<210> 56

<211> 68

<212> PRT

<213> Bacillus licheniformis

<400> 56

Met Gly Val Asp Val Asn Ile Ile Phe Gln Ile Ala Gly Val Gly Ile
1   5   10   15

Page 85

Val Val Ala Phe Leu His Thr Ile Leu Asp Gln Met Gly Lys Lys Glu
                20   25   30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
        35   40   45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
    50   55   60

Leu Phe Gln Gly
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<210> 57

<211> 85

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<213> Bacillus licheniformis

<400> 57

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Ser Leu Ile Val Lys Glu Gln Lys Pro Thr Phe Ala Phe Leu Ile Val
                20   25   30

Val Phe Ala Gly Cys Thr Ile Phe Leu Phe Leu Val Asp Gln Val Tyr
        35   40   45

Glu Ile Ile Arg Met Ile Glu Lys Ile Ala Ala Asn Ala Asn Ile Asn
    50   55   60

Met Met Tyr Val Glu Thr Ile Leu Lys Ile Ile Gly Ile Ala Tyr Ile
65   70   75   80

Ala Glu Phe Gly Ala
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<210> 58

<211> 1207

<212> DNA

<213> Bacillus licheniformis

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<222> (501)..(704)

Page 86

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ccgtcaggca tcaaaacaga tcgcacacca gcttaccgag ccggtagcct ctttgtttca     180

gacatttgca gaacagcttg aaaaaggcag cgcttcagca gggacggcat gggaagacag     240

cctggagaaa gtatggcccg aaacggctct taaaaagaaa gaatacgaga ttttacggca     300

attcggcgaa acgctgggcc gtcatgatct gatttctcag caaaaacata tcaaactggc     360

gttaacccat ttagagacag aggaagctga agcaaatctc gcccaggcga aaaatgaaaa     420

aatggtcaaa agccttggat ttttgacggg actgctactg attcttctat tgatgtaatg     480

aagaggggag catacacgaa atg gga gta gac gta aat att att ttt caa att     533
                      Met Gly Val Asp Val Asn Ile Ile Phe Gln Ile
                       1               5                  10

gcc ggc gtc ggg atc gtc gtc gct ttt ctt cac acc ata ctg gat caa     581
Ala Gly Val Gly Ile Val Val Ala Phe Leu His Thr Ile Leu Asp Gln
                15                  20                  25

atg ggg aag aag gaa tat gcc caa tgg gtc acg ctt tta gga ttc att     629
Met Gly Lys Lys Glu Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile
            30                  35                  40

tat ata ttg ttc atg gtg gca act gtt gtc gat gat cta ttc caa aag     677
Tyr Ile Leu Phe Met Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys
        45                  50                  55

ata aaa gct gtc ttt cta ttt caa gga tagggggct cactcattga            724
Ile Lys Ala Val Phe Leu Phe Gln Gly
60                  65

aatcgttcaa atcgtaggac tgggaatgat cgccaccttc ctcagcttga ttgtgaaaga     784

gcaaaaaccg acgtttgctt ttttgattgt cgtttttgcc ggctgcacga tttttttatt     844

cttagtagat caggtctacg aaatcattcg gatgattgaa aaaatagctg ccaatgccaa     904

catcaacatg atgtatgtcg aaacgatttt gaagattatc gggattgctt atattgcgga     964

gtttggcgcc cagctgacaa aggatgccgg acagggtgcg attgcttcga agatcgaatt    1024

ggcaggcaaa atcctcatct tagtcatggc tgtgcctatt ttaaccgtga ttatcgaaac    1084

gatcatcgga ctcatccctt ccatgtctta gtcagaaagg aggatttcct gagtgaagcg    1144

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<213> Bacillus licheniformis

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Val Val Ala Phe Leu His Thr Ile Leu Asp Gln Met Gly Lys Lys Glu
            20   25   30

Tyr Ala Gln Trp Val Thr Leu Leu Gly Phe Ile Tyr Ile Leu Phe Met
        35   40   45

Val Ala Thr Val Val Asp Asp Leu Phe Gln Lys Ile Lys Ala Val Phe
    50   55   60

Leu Phe Gln Gly
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<210> 60

<211> 2153

<212> DNA

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ccaccttcct cagcttgatt gtgaaagagc aaaaaccgac gtttgctttt ttgattgtcg   180
tttttgccgg ctgcacgatt tttttattct tagtagatca ggtctacgaa atcattcgga   240
tgattgaaaa aatagctgcc aatgccaaca tcaacatgat gtatgtcgaa acgattttga   300
agattatcgg gattgcttat attgcggagt ttggcgccca gctgacaaag gatgccggac   360
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cagaaaggag gatttcctga gtg aag cgt ttt ctg ttc tgg ctc ttg gtc atc   533
                         Val Lys Arg Phe Leu Phe Trp Leu Leu Val Ile
                          1   5   10

gga atc gta tgc ttt gga gcg cat aat gta caa gct tcg cca aaa gaa   581
Gly Ile Val Cys Phe Gly Ala His Asn Val Gln Ala Ser Pro Lys Glu
             15   20   25

Page 88

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gcg gag ccg gct ggg gaa acc gct gca gaa gaa tcg gca gaa gcc att       629
Ala Glu Pro Ala Gly Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile
        30              35                  40

gca aga gag cag gct gaa ggt ttg gaa cta gac cgg gtc ggg gag ttc       677
Ala Arg Glu Gln Ala Glu Gly Leu Glu Leu Asp Arg Val Gly Glu Phe
 45              50                  55

tgg aac aac att ttg aca gag tat ggg gga cac ctt ccc gaa agt caa       725
Trp Asn Asn Ile Leu Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln
60              65                  70                  75

aaa gga agc ctg ctt gaa ttt gtc aaa gga gaa aag cac ttt tcg cct       773
Lys Gly Ser Leu Leu Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro
                80                  85                  90

gag gaa tgg ggc aaa gcg ctg ttt tcc tac ttg ttc cat gaa gtg ctg       821
Glu Glu Trp Gly Lys Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu
            95                  100                 105

gct aac ggg aaa ctg ctg ggg acg ctg atc ctg ttg acc atc ttc tgc       869
Ala Asn Gly Lys Leu Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys
        110                 115                 120

gtc ctg ctt cag ctt ttg caa aac gcg ttt caa caa agc acc gtc agc       917
Val Leu Leu Gln Leu Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser
        125                 130                 135

aaa gtg gcg tat gca att gtc tac atg gtg ctg att att ctt gcg ctc       965
Lys Val Ala Tyr Ala Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu
140                 145                 150                 155

aac agc ttt cgg gtt gcc gtc aca tat gcg aat gaa gcg att cag acg      1013
Asn Ser Phe Arg Val Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr
                160                 165                 170

atg aca agc ttt atc ctg tcg ctc gta cct ctg ctt ctg gcg ctg atg      1061
Met Thr Ser Phe Ile Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met
                175                 180                 185

gcg act tcg ggg gga gcc gcc tca gcc gca ttc ttt cat ccg gtc att      1109
Ala Thr Ser Gly Gly Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile
        190                 195                 200

ctt ttt ctc atg aac acg agc ggc ttg ttt atc caa tat atc gtg ttg      1157
Leu Phe Leu Met Asn Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu
        205                 210                 215

ccg ctt tta ttt tta tca gcg att tta agc att gtc agc acg atg acg      1205
Pro Leu Leu Phe Leu Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr
220                 225                 230                 235

gac caa tat aaa gtc aca cag ctg gcc cag ctc ctc aga aat gcg gcg      1253
Asp Gln Tyr Lys Val Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala
                240                 245                 250

atc ggc acg ctg gct gca ttt ttg acc gta ttc ctc ggt gtc atc tcg      1301
Ile Gly Thr Leu Ala Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser
                255                 260                 265

gtt cag ggc gcc tca gcc gca gtg acg gac ggc att act ttg cgg acg      1349
Val Gln Gly Ala Ser Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr
        270                 275                 280

gca aaa ttc att acc gga aac ttc atc ccc gta ttg ggc cgc atg ttt      1397
Ala Lys Phe Ile Thr Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe
285                 290                 295
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Page 89

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acc gaa gcg aca gac acg gtg atc agc gcg tct ctc ctg ctg aaa aac    1445
Thr Glu Ala Thr Asp Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn
300               305               310               315

acc gtc ggg ata ctc ggt gtg gca atc tta att tgc atc gca gcc ttt    1493
Thr Val Gly Ile Leu Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe
320               325               330

ccc gcg atc aaa atc ctt tcc ctc gcg ctc ata tac aaa att gcc gcg    1541
Pro Ala Ile Lys Ile Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala
335               340               345

gcg gtt ctc cag cct ctc gga ggc ggc ccg gtt atc agc tgc ctg gat    1589
Ala Val Leu Gln Pro Leu Gly Gly Gly Pro Val Ile Ser Cys Leu Asp
350               355               360

gtc atc agc aaa agc gtc atc tac att ttc gcg gcc atg gcc atc gtt    1637
Val Ile Ser Lys Ser Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val
365               370               375

tcg ctg atg ttt ttc tta agc tta acc gtg atc att aca gcg ggg aat    1685
Ser Leu Met Phe Phe Leu Ser Leu Thr Val Ile Ile Thr Ala Gly Asn
380               385               390               395

ctg acg atg atg atg aag tagggaggga tgagatggaa tttctgacag           1733
Leu Thr Met Met Met Lys
400
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agtggctcac gaatattatt ctatttattc tgatggcgat cgtcatcgat atgcttctgc   1793

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tactgaaccc gatcttctct ttattcagga cagatccgga tgtgattttt gagaagctta   1913

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aaatacaagc ctcacaacaa gcatatatct tagaacagat ggctgttcaa ttggaaaaga   2033

acgcagaggg caggtttaca agcgacaaat acaagataga ccgagtcgag gtctcttctg   2093

acagccagct gaaaacagag aaagacctca gtaagcatgc ggaagtctcg gtattcttga   2153

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<213> Bacillus licheniformis

<400> 61

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Gly Ala His Asn Val Gln Ala Ser Pro Lys Glu Ala Glu Pro Ala Gly
20               25               30

Glu Thr Ala Ala Glu Glu Ser Ala Glu Ala Ile Ala Arg Glu Gln Ala
35               40               45
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Page 90

Glu Gly Leu Glu Leu Asp Arg Val Gly Glu Phe Trp Asn Asn Ile Leu
50   55   60

Thr Glu Tyr Gly Gly His Leu Pro Glu Ser Gln Lys Gly Ser Leu Leu
65   70   75   80

Glu Phe Val Lys Gly Glu Lys His Phe Ser Pro Glu Glu Trp Gly Lys
                    85   90   95

Ala Leu Phe Ser Tyr Leu Phe His Glu Val Leu Ala Asn Gly Lys Leu
                    100   105   110

Leu Gly Thr Leu Ile Leu Leu Thr Ile Phe Cys Val Leu Leu Gln Leu
                    115   120   125

Leu Gln Asn Ala Phe Gln Gln Ser Thr Val Ser Lys Val Ala Tyr Ala
                    130   135   140

Ile Val Tyr Met Val Leu Ile Ile Leu Ala Leu Asn Ser Phe Arg Val
145   150   155   160

Ala Val Thr Tyr Ala Asn Glu Ala Ile Gln Thr Met Thr Ser Phe Ile
                    165   170   175

Leu Ser Leu Val Pro Leu Leu Leu Ala Leu Met Ala Thr Ser Gly Gly
                    180   185   190

Ala Ala Ser Ala Ala Phe Phe His Pro Val Ile Leu Phe Leu Met Asn
                    195   200   205

Thr Ser Gly Leu Phe Ile Gln Tyr Ile Val Leu Pro Leu Leu Phe Leu
210   215   220

Ser Ala Ile Leu Ser Ile Val Ser Thr Met Thr Asp Gln Tyr Lys Val
225   230   235   240

Thr Gln Leu Ala Gln Leu Leu Arg Asn Ala Ala Ile Gly Thr Leu Ala
                    245   250   255

Ala Phe Leu Thr Val Phe Leu Gly Val Ile Ser Val Gln Gly Ala Ser
                    260   265   270

Ala Ala Val Thr Asp Gly Ile Thr Leu Arg Thr Ala Lys Phe Ile Thr
                    275   280   285

Gly Asn Phe Ile Pro Val Leu Gly Arg Met Phe Thr Glu Ala Thr Asp
                    290   295   300

Thr Val Ile Ser Ala Ser Leu Leu Leu Lys Asn Thr Val Gly Ile Leu
305   310   315   320

Page 91

Gly Val Ala Ile Leu Ile Cys Ile Ala Ala Phe Pro Ala Ile Lys Ile
325   330   335

Leu Ser Leu Ala Leu Ile Tyr Lys Ile Ala Ala Ala Val Leu Gln Pro
340   345   350

Leu Gly Gly Gly Pro Val Ile Ser Cys Leu Asp Val Ile Ser Lys Ser
355   360   365

Val Ile Tyr Ile Phe Ala Ala Met Ala Ile Val Ser Leu Met Phe Phe
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Lys

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agggggagaa cgaagcggca atg aat aaa aga acc tgg atc gaa aag ctg atc   533
                        Met Asn Lys Arg Thr Trp Ile Glu Lys Leu Ile
                        1   5   10

ggc cac ctg ctc ccg aaa gac gag aaa gac gga aaa aag ctg acg aaa   581
Gly His Leu Leu Pro Lys Asp Glu Lys Asp Gly Lys Lys Leu Thr Lys
            15   20   25

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Tyr His Tyr Phe Leu Leu Leu Phe Val Leu Gly Val Ser Phe Met Leu
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gtc agc cag atc ttc tct tcc gaa cct tcc caa gag cca gcg gca gat      677
Val Ser Gln Ile Phe Ser Ser Glu Pro Ser Gln Glu Pro Ala Ala Asp
        45              50                  55

cag ccg gcg gct tca caa aaa gct acg tct gaa agc acc gta cag agc      725
Gln Pro Ala Ala Ser Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser
60              65                  70                  75

ggt gaa gga gaa aaa gaa gtg ttc aag ccc gcc tca gat gac aaa ccg      773
Gly Glu Gly Glu Lys Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro
                80              85                  90

aag gaa tcg atc caa gat tac gaa cag gaa tat gaa aat cag ctc aaa      821
Lys Glu Ser Ile Gln Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys
                95              100                 105

gac ata ttg gaa acc atc atc ggc gtt gag gac gtg tca atc gtc gtc      869
Asp Ile Leu Glu Thr Ile Ile Gly Val Glu Asp Val Ser Ile Val Val
        110             115                 120

aat gtt gat gca acc tca ttg aaa ata ttc gag aaa aac aga aaa acc      917
Asn Val Asp Ala Thr Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr
        125             130                 135

cag gaa act tca acg aat gag aca gat aaa cag gga ggc aag cgg acg      965
Gln Glu Thr Ser Thr Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr
140             145                 150                 155

gtg tct gaa atg tct tca gac gaa gaa atc gtc atc atc aaa aac gga     1013
Val Ser Glu Met Ser Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly
                160             165                 170

gat aaa gag acg cct gtc gtc gtt cag acg aaa aag ccc gat atc agg     1061
Asp Lys Glu Thr Pro Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg
                175             180                 185

ggt gtt ctc gtt gtc gct cag gga gtc gac aac gtt caa ata aaa aag     1109
Gly Val Leu Val Val Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys
                190             195                 200

acc att att gaa gca gtg aca agg gtt ctt gat gtt ccg agc cac cgc     1157
Thr Ile Ile Glu Ala Val Thr Arg Val Leu Asp Val Pro Ser His Arg
205             210                 215

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Val Ala Val Ala Pro Lys Lys Met Lys Glu Asp Ser
220             225                 230

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Page 93

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<212> PRT

<213> Bacillus licheniformis

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Leu Leu Phe Val Leu Gly Val Ser Phe Met Leu Val Ser Gln Ile Phe
            35   40   45

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        50   55   60

Gln Lys Ala Thr Ser Glu Ser Thr Val Gln Ser Gly Glu Gly Glu Lys
65   70   75   80

Glu Val Phe Lys Pro Ala Ser Asp Asp Lys Pro Lys Glu Ser Ile Gln
                85   90   95

Asp Tyr Glu Gln Glu Tyr Glu Asn Gln Leu Lys Asp Ile Leu Glu Thr
            100   105   110

Ile Ile Gly Val Glu Asp Val Ser Ile Val Val Asn Val Asp Ala Thr
        115   120   125

Ser Leu Lys Ile Phe Glu Lys Asn Arg Lys Thr Gln Glu Thr Ser Thr
    130   135   140

Asn Glu Thr Asp Lys Gln Gly Gly Lys Arg Thr Val Ser Glu Met Ser
145   150   155   160

Ser Asp Glu Glu Ile Val Ile Ile Lys Asn Gly Asp Lys Glu Thr Pro
                165   170   175

Val Val Val Gln Thr Lys Lys Pro Asp Ile Arg Gly Val Leu Val Val
            180   185   190

Ala Gln Gly Val Asp Asn Val Gln Ile Lys Lys Thr Ile Ile Glu Ala
        195   200   205

Page 94

Val Thr Arg Val Leu Asp Val Pro Ser His Arg Val Ala Val Ala Pro
     210   215   220

Lys Lys Met Lys Glu Asp Ser
225   230

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<211>   1062

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caacctcatt gaaaatattc gagaaaaaca gaaaacccca ggaaacttca acgaatgaga   240

cagataaaca gggaggcaag cggacggtgt ctgaaatgtc ttcagacgaa gaaatcgtca   300

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ggggtgttct cgttgtcgct cagggagtcg acaacgttca ataaaaaag accattattg   420

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                   Met Met Leu Lys Lys Gln Thr Val Trp Leu Leu
                   1   5   10

acc atg tta agt ctc gtc gtt gta ctg agt gtc tac tac att atg tcg   578
Thr Met Leu Ser Leu Val Val Val Leu Ser Val Tyr Tyr Ile Met Ser
          15   20   25

ccc gaa gga gaa aat gtc gtc acg gtt gat gac aag gaa caa gtt gcc   626
Pro Glu Gly Glu Asn Val Val Thr Val Asp Asp Lys Glu Gln Val Ala
          30   35   40

gct gaa aaa gaa aaa ccg atg aaa gaa gag cct gcc aag gat ggc aaa   674
Ala Glu Lys Glu Lys Pro Met Lys Glu Glu Pro Ala Lys Asp Gly Lys
          45   50   55

gat gat acc gcg cct gct aaa gac aaa act aaa ggg aaa gat aca aaa   722
Asp Asp Thr Ala Pro Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys
60   65   70   75

gat aaa gaa acg tct gcg agt gag cag aac gga gag gtt gtc aca gag   770
Asp Lys Glu Thr Ser Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu
               80   85   90

Page 95

```
gaa tca tcg ggt gat gaa gat tta ttc aca aca tac cgc atg gaa atg      818
Glu Ser Ser Gly Asp Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met
            95              100                 105

gac gat cag cgc agc agg gag agg gag gaa tta acc gaa atc gtc aga      866
Asp Asp Gln Arg Ser Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg
        110             115                 120

agc gat aaa gcg acg gca aaa gaa aaa agc gaa gct tac gac aag atg      914
Ser Asp Lys Ala Thr Ala Lys Glu Lys Ser Glu Ala Tyr Asp Lys Met
    125             130                 135

aca gag ctc agc gaa gct gaa gga acg gaa aag acc ctt gaa acc ctc      962
Thr Glu Leu Ser Glu Ala Glu Gly Thr Glu Lys Thr Leu Glu Thr Leu
140             145                 150                 155

atc aaa aca aaa ggc tat taagacgcct tggtcaacgc cgacggcgat           1010
Ile Lys Thr Lys Gly Tyr
                160

aaagtcaata ttacggtgaa ggcgaaggag cactcgaaag ccgcctgcac cg          1062
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<210> 65

<211> 161

<212> PRT

<213> Bacillus licheniformis

<400> 65

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Met Met Leu Lys Lys Gln Thr Val Trp Leu Leu Thr Met Leu Ser Leu
1               5               10                  15

Val Val Val Leu Ser Val Tyr Tyr Ile Met Ser Pro Glu Gly Glu Asn
            20              25                  30

Val Val Thr Val Asp Asp Lys Glu Gln Val Ala Ala Glu Lys Glu Lys
        35              40                  45

Pro Met Lys Glu Glu Pro Ala Lys Asp Gly Lys Asp Asp Thr Ala Pro
    50              55                  60

Ala Lys Asp Lys Thr Lys Gly Lys Asp Thr Lys Asp Lys Glu Thr Ser
65              70              75                  80

Ala Ser Glu Gln Asn Gly Glu Val Val Thr Glu Glu Ser Ser Gly Asp
            85              90                  95

Glu Asp Leu Phe Thr Thr Tyr Arg Met Glu Met Asp Asp Gln Arg Ser
            100             105                 110

Arg Glu Arg Glu Glu Leu Thr Glu Ile Val Arg Ser Asp Lys Ala Thr
        115             120                 125
```

Page 96

```
Ala Lys Glu Lys Ser Glu Ala Tyr Asp Lys Met Thr Glu Leu Ser Glu
    130                 135                 140

Ala Glu Gly Thr Glu Lys Thr Leu Glu Thr Leu Ile Lys Thr Lys Gly
145                 150                 155                 160

Tyr
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<210> 66

<211> 3346

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(2843)

<223>


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taaatacgga ttaatcgatg aaaaccggcg agagacagac aggcgattca aaagctgatg    120

aatataatcg aacaaaacaa ggacgcacag gaagagataa tccaatgatt ctgtataaaa    180

aaatgccgca ggaaatcgtg ttcgcagggc aggcggaaaa ctcgaactta aaacagatcg    240

atgtaaacag cgtaccactt ttagtcgaga tgaacggaga ggaagcaagg aacgttcaga    300

gttctcagca cgaacccgat ggattttta aaacaagaaa cggcccctgg gcagacgctt    360

aaactgacat tttataaata gctggagtgt ctcaaggata aatatgctat aataggggaa    420

tccagaggaa aatcgcagcc gaaaaaaggc tgctttctct ttgtttttac atttttaac    480

acgcagtaag gtgatggaac atg gca aaa aga aaa cga aaa tca aca aag aaa    533
                       Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys
                         1               5                  10

caa aaa caa gga aaa aaa cgg atc cat ctt aaa ttt gaa ttg tac gga    581
Gln Lys Gln Gly Lys Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly
            15                  20                  25

tta atc tgt atc gcc atc tcg att att gcg gtt ttg cag ctt ggc gta    629
Leu Ile Cys Ile Ala Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val
        30                  35                  40

gca ggg caa acg ttc att tac atg ttc cgc ttt ttc gcc ggt gaa tgg    677
Ala Gly Gln Thr Phe Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp
        45                  50                  55

ttc atc ctt tgc ctt ctc ggc ctc ttt tta acg ggc ttg tct tta ttt    725
Phe Ile Leu Cys Leu Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe
60                  65                  70                  75
```

```
tgg aaa aag aaa aca ccc agt ttt ttg acg agg aga aaa gcg ggc ctt        773
Trp Lys Lys Lys Thr Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu
            80                  85                  90

tac tgc atc att gca agc atg ctg ctt ctt tca cat gtc cag ctg ttt        821
Tyr Cys Ile Ile Ala Ser Met Leu Leu Leu Ser His Val Gln Leu Phe
            95                 100                 105

cag cat ttg acc gaa agg gga atg gtt cag tct ccg agc gtg atc caa        869
Gln His Leu Thr Glu Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln
            110                115                 120

aat acg tgg gag ctg ttt ctg atg gat gta aaa ggc gag aca gga tcg        917
Asn Thr Trp Glu Leu Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser
        125                130                 135

cct gat ctt gga ggc gga atg att gga gcc ctt tta ttc gcg gcg tca        965
Pro Asp Leu Gly Gly Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser
140                 145                 150                 155

tat ttt ctg ttt gca tct gca gga tct aaa atc atc gcc gtc ttc ctg       1013
Tyr Phe Leu Phe Ala Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu
                160                 165                 170

atc ttg atc ggc ctt ctt ttg att acg gat cgg tcg ctt cag gag acg       1061
Ile Leu Ile Gly Leu Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr
                175                 180                 185

ctg atc aaa tgg atg acc ccg gtc gcc tcc ttc atg aaa aac cag tgg       1109
Leu Ile Lys Trp Met Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp
            190                 195                 200

cag gcc ttt tta gca gat ctt aaa caa ttg aaa aac agc tcg ccg aaa       1157
Gln Ala Phe Leu Ala Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys
        205                 210                 215

aag aaa tcc gga aaa aaa caa aag acg cag aga aaa ccg aaa gtg tct       1205
Lys Lys Ser Gly Lys Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser
220                 225                 230                 235

gaa gag cct gta caa gaa gcg gac ctt gat cca gat ccg gtt att caa       1253
Glu Glu Pro Val Gln Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln
                240                 245                 250

tca gaa ccg att att tca agc ttt tcc gac cgt gat gaa aag ccc gaa       1301
Ser Glu Pro Ile Ile Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu
                255                 260                 265

gtt caa gct tac gaa gct ccg gcg gct cct gct gaa cct cct gct gag       1349
Val Gln Ala Tyr Glu Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu
        270                 275                 280

ccc gaa atc ggt gag gaa atg cag gcc tcc ggc gcg ccc gaa atc acg       1397
Pro Glu Ile Gly Glu Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr
        285                 290                 295

ttt aca gag cta gaa aac aag gat tac cag ctt ccg tcg att caa ttg       1445
Phe Thr Glu Leu Glu Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu
300                 305                 310                 315

ctg gat gat ccg aag cac aca ggg cag cag gcg gat aaa aag aat att       1493
Leu Asp Asp Pro Lys His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile
                320                 325                 330

tac gac aat gcc agg aag ctg gaa agg acg ttt caa agc ttc gga gtt       1541
Tyr Asp Asn Ala Arg Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val
        335                 340                 345
```

Page 98

```
aag gcg aaa gtc acc cag gtt cat ctc ggc ccg gcc gtc acg aaa tat    1589
Lys Ala Lys Val Thr Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr
        350                 355                 360

gaa gtc tat cct gat gtg ggc gtc aaa gtc agc aaa att gtc aac tta    1637
Glu Val Tyr Pro Asp Val Gly Val Lys Val Ser Lys Ile Val Asn Leu
        365                 370                 375

agt gac gac ttg gct tta gcg ctc gcg gcc aag gat atc cgc atc gaa    1685
Ser Asp Asp Leu Ala Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu
380                 385                 390                 395

gcc ccg atc ccc gga aaa tcg gcg att gga atc gaa gtg ccg aat gcg    1733
Ala Pro Ile Pro Gly Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala
                400                 405                 410

gaa gtg gcg atg gtt tcc ttg aaa gaa gtg ctt gaa tcg aaa ctg aat    1781
Glu Val Ala Met Val Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn
                415                 420                 425

gac cgg ccg gat gca aag ctg atg atc ggc ctc ggc cgg aac att tcc    1829
Asp Arg Pro Asp Ala Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser
                430                 435                 440

gga gaa gcg gta ttg gca gag ctg aac aaa atg ccc cac ctt ctt gtt    1877
Gly Glu Ala Val Leu Ala Glu Leu Asn Lys Met Pro His Leu Leu Val
        445                 450                 455

gca gga gcg acc gga agc ggg aaa agc gtc tgt gtc aac ggg atc att    1925
Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile
460                 465                 470                 475

aca agc att ttg atg agg gca aag ccc cac gaa gtg aag atg atg atg    1973
Thr Ser Ile Leu Met Arg Ala Lys Pro His Glu Val Lys Met Met Met
                480                 485                 490

att gat ccg aaa atg gtc gag ctc aat gtc tac aac ggg att ccg cat    2021
Ile Asp Pro Lys Met Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His
                495                 500                 505

ttg ctc gct ccc gtc gtg aca gac ccg aaa aaa gca tcg cag gct ttg    2069
Leu Leu Ala Pro Val Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu
                510                 515                 520

aag aaa gtc gtc aac gaa atg gag cgg cgc tac gaa ttg ttt tct cac    2117
Lys Lys Val Val Asn Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His
        525                 530                 535

acg gga acg aga aat atc gaa ggg tat aac gac tat att aaa cgg atg    2165
Thr Gly Thr Arg Asn Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met
540                 545                 550                 555

aat gcc gca gaa gaa gca aag cag ccg gag ctt cca tac atc att gtg    2213
Asn Ala Ala Glu Glu Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val
                560                 565                 570

att gtg gac gag ctt gcc gac ctg atg atg gtc gct tcc tct gat gtt    2261
Ile Val Asp Glu Leu Ala Asp Leu Met Met Val Ala Ser Ser Asp Val
                575                 580                 585

gaa gac tcg atc aca agg ctt tcg caa atg gcc agg gcg gcg ggc atc    2309
Glu Asp Ser Ile Thr Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile
                590                 595                 600

cac ctg atc att gcg acg cag agg cct tcg gtc gat gtt atc aca ggg    2357
His Leu Ile Ile Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly
                605                 610                 615
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gtc att aaa gcc aac att ccg tca agg atc gct ttc agc gta tcg tct    2405
Val Ile Lys Ala Asn Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser
620             625             630             635

cag acc gac tcc agg acg att ctt gat atg gga ggc gct gaa aaa ctt    2453
Gln Thr Asp Ser Arg Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu
            640             645             650

ctc ggc aga ggg gac atg ctg ttt ctc cct gtc ggc gcc aat aaa ccg    2501
Leu Gly Arg Gly Asp Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro
        655             660             665

ctc cgc gtt caa ggt gcc ttt ctg tca gac gaa gaa gtt gaa aaa gtt    2549
Leu Arg Val Gln Gly Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val
        670             675             680

gtc gat cac gtc atc agc cag caa aaa gcc caa tac caa gaa gaa atg    2597
Val Asp His Val Ile Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met
    685             690             695

att cca gaa gag acg cag gaa acg gtc agc gaa gtg aca gac gac ctt    2645
Ile Pro Glu Glu Thr Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu
700             705             710             715

tat gac gaa gcg gtc gca ctt gtg gtc agc atg cag acg gct tct gta    2693
Tyr Asp Glu Ala Val Ala Leu Val Val Ser Met Gln Thr Ala Ser Val
            720             725             730

tcc atg ctg caa agg aga ttc cgc atc ggc tat aca aga gcg gcg cgg    2741
Ser Met Leu Gln Arg Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg
        735             740             745

ctt atc gat gcc atg gaa gag cgg gga atc gtc ggc cca tat gaa gga    2789
Leu Ile Asp Ala Met Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly
        750             755             760

tca aaa ccc cgt gaa gtt ctc ttg tca aaa gag caa tac gaa gaa ctc    2837
Ser Lys Pro Arg Glu Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu
765             770             775

tct tct tgagaagaga gttcttgttt aacataattt cattatgtaa actaaaaaac    2893
Ser Ser
780

atctatttat ttatttgaca aaacatgata tagttatcct caattaaaga taatttgaat    2953

ctgatctgtc agacggaggg aaaacatgtc gataaaagct gacaatcaac ggttatgttt    3013

aaaggtgatt gatcggataa aagatgatat tcaaaatggg gtcttttgcg aaaatgaacg    3073

gctcccgagt gaatttgagc tgtcaaagat gcttggtgtg agcagaacgg ctttgcgtga    3133

ggcgcttaga atactggaag aagaaaacgt catcatcaga aggcatggag tcggacattt    3193

tgtaaatgcc agaccgttat ttctatcagg tattgagcag ctgaacagcg tcacaaaaat    3253

gatcgagcag gcaagcatga cgccgggaac catttttatg tcctcacagg ttaccgctcc    3313

cactgaagaa gatatgctcc ggtttcaata tgc    3346
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<210>   67

<211>   781

<212>   PRT

<213>   Bacillus licheniformis

<400>   67

Met Ala Lys Arg Lys Arg Lys Ser Thr Lys Lys Gln Lys Gln Gly Lys
1   5   10   15

Lys Arg Ile His Leu Lys Phe Glu Leu Tyr Gly Leu Ile Cys Ile Ala
                20   25   30

Ile Ser Ile Ile Ala Val Leu Gln Leu Gly Val Ala Gly Gln Thr Phe
            35   40   45

Ile Tyr Met Phe Arg Phe Phe Ala Gly Glu Trp Phe Ile Leu Cys Leu
        50   55   60

Leu Gly Leu Phe Leu Thr Gly Leu Ser Leu Phe Trp Lys Lys Lys Thr
65   70   75   80

Pro Ser Phe Leu Thr Arg Arg Lys Ala Gly Leu Tyr Cys Ile Ile Ala
                85   90   95

Ser Met Leu Leu Leu Ser His Val Gln Leu Phe Gln His Leu Thr Glu
                100   105   110

Arg Gly Met Val Gln Ser Pro Ser Val Ile Gln Asn Thr Trp Glu Leu
            115   120   125

Phe Leu Met Asp Val Lys Gly Glu Thr Gly Ser Pro Asp Leu Gly Gly
    130   135   140

Gly Met Ile Gly Ala Leu Leu Phe Ala Ala Ser Tyr Phe Leu Phe Ala
145   150   155   160

Ser Ala Gly Ser Lys Ile Ile Ala Val Phe Leu Ile Leu Ile Gly Leu
                165   170   175

Leu Leu Ile Thr Asp Arg Ser Leu Gln Glu Thr Leu Ile Lys Trp Met
                180   185   190

Thr Pro Val Ala Ser Phe Met Lys Asn Gln Trp Gln Ala Phe Leu Ala
            195   200   205

Asp Leu Lys Gln Leu Lys Asn Ser Ser Pro Lys Lys Lys Ser Gly Lys
    210   215   220

Lys Gln Lys Thr Gln Arg Lys Pro Lys Val Ser Glu Glu Pro Val Gln
225   230   235   240

Glu Ala Asp Leu Asp Pro Asp Pro Val Ile Gln Ser Glu Pro Ile Ile
                245   250   255

Ser Ser Phe Ser Asp Arg Asp Glu Lys Pro Glu Val Gln Ala Tyr Glu
          260   265   270

Ala Pro Ala Ala Pro Ala Glu Pro Pro Ala Glu Pro Glu Ile Gly Glu
          275   280   285

Glu Met Gln Ala Ser Gly Ala Pro Glu Ile Thr Phe Thr Glu Leu Glu
    290   295   300

Asn Lys Asp Tyr Gln Leu Pro Ser Ile Gln Leu Leu Asp Asp Pro Lys
305   310   315   320

His Thr Gly Gln Gln Ala Asp Lys Lys Asn Ile Tyr Asp Asn Ala Arg
          325   330   335

Lys Leu Glu Arg Thr Phe Gln Ser Phe Gly Val Lys Ala Lys Val Thr
          340   345   350

Gln Val His Leu Gly Pro Ala Val Thr Lys Tyr Glu Val Tyr Pro Asp
          355   360   365

Val Gly Val Lys Val Ser Lys Ile Val Asn Leu Ser Asp Asp Leu Ala
    370   375   380

Leu Ala Leu Ala Ala Lys Asp Ile Arg Ile Glu Ala Pro Ile Pro Gly
385   390   395   400

Lys Ser Ala Ile Gly Ile Glu Val Pro Asn Ala Glu Val Ala Met Val
          405   410   415

Ser Leu Lys Glu Val Leu Glu Ser Lys Leu Asn Asp Arg Pro Asp Ala
          420   425   430

Lys Leu Met Ile Gly Leu Gly Arg Asn Ile Ser Gly Glu Ala Val Leu
          435   440   445

Ala Glu Leu Asn Lys Met Pro His Leu Leu Val Ala Gly Ala Thr Gly
    450   455   460

Ser Gly Lys Ser Val Cys Val Asn Gly Ile Ile Thr Ser Ile Leu Met
465   470   475   480

Arg Ala Lys Pro His Glu Val Lys Met Met Met Ile Asp Pro Lys Met
          485   490   495

Val Glu Leu Asn Val Tyr Asn Gly Ile Pro His Leu Leu Ala Pro Val
          500   505   510

Val Thr Asp Pro Lys Lys Ala Ser Gln Ala Leu Lys Lys Val Val Asn
          515   520   525

Glu Met Glu Arg Arg Tyr Glu Leu Phe Ser His Thr Gly Thr Arg Asn
    530   535   540

Ile Glu Gly Tyr Asn Asp Tyr Ile Lys Arg Met Asn Ala Ala Glu Glu
545   550   555   560

Ala Lys Gln Pro Glu Leu Pro Tyr Ile Ile Val Ile Val Asp Glu Leu
            565   570   575

Ala Asp Leu Met Met Val Ala Ser Ser Asp Val Glu Asp Ser Ile Thr
            580   585   590

Arg Leu Ser Gln Met Ala Arg Ala Ala Gly Ile His Leu Ile Ile Ala
        595   600   605

Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Val Ile Lys Ala Asn
    610   615   620

Ile Pro Ser Arg Ile Ala Phe Ser Val Ser Ser Gln Thr Asp Ser Arg
625   630   635   640

Thr Ile Leu Asp Met Gly Gly Ala Glu Lys Leu Leu Gly Arg Gly Asp
            645   650   655

Met Leu Phe Leu Pro Val Gly Ala Asn Lys Pro Leu Arg Val Gln Gly
            660   665   670

Ala Phe Leu Ser Asp Glu Glu Val Glu Lys Val Val Asp His Val Ile
        675   680   685

Ser Gln Gln Lys Ala Gln Tyr Gln Glu Glu Met Ile Pro Glu Glu Thr
    690   695   700

Gln Glu Thr Val Ser Glu Val Thr Asp Asp Leu Tyr Asp Glu Ala Val
705   710   715   720

Ala Leu Val Val Ser Met Gln Thr Ala Ser Val Ser Met Leu Gln Arg
            725   730   735

Arg Phe Arg Ile Gly Tyr Thr Arg Ala Ala Arg Leu Ile Asp Ala Met
            740   745   750

Glu Glu Arg Gly Ile Val Gly Pro Tyr Glu Gly Ser Lys Pro Arg Glu
        755   760   765

Val Leu Leu Ser Lys Glu Gln Tyr Glu Glu Leu Ser Ser
    770   775   780

<210> 68

<211> 1045

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1043)

<223>

<400> 68
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atcaatgaac ctgtcatttt cggacttccg gtcgtgctca atccaatctt catgattccc     120

tttattatcg ttccggcagt caatactgtc atcggctatt tgttcatcaa gtttcagctg     180

attccgccga tcgcatacgc tgttccgtgg acaacgccag ggccgttgat tccgtttctc     240

gggaccggag gaaactggct tgcgctcggc gtcggctttc tctgcctcgc catttcaacg     300

atgatttatc tgccgtttgt gatggctgcc aacaagactg tgaatacgga cagggagcat     360

tccgcggaaa acaggaagga atcataactt tagacggggc gccttttacg ggcgcccgtc     420

ttttttaaa aaaagtcatg cggctctctt ttctctcata caatctatta aaatcaaaag     480

cacgtctggg aggaagatac atg cgg aag ccc aca atc aaa gag ctc atc ttt     533
                        Met Arg Lys Pro Thr Ile Lys Glu Leu Ile Phe
                        1               5                   10

caa cat atg aag gac cat ctg tcg atc tat tta ttt gtt tct gtg ctg     581
Gln His Met Lys Asp His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu
                15                  20                  25

ttc tta atg ggt gtg att ttc ggc gcg gtc atc gtc aac agc atg acg     629
Phe Leu Met Gly Val Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr
            30                  35                  40

atc ggt caa aaa gaa gat ttg ttc tac tat ttg aat caa ttt ttt gga     677
Ile Gly Gln Lys Glu Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly
    45                  50                  55

cag ctt tcc gaa gga aaa gca gcc agc tca aag gaa atg ttt ttg cag     725
Gln Leu Ser Glu Gly Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln
60                  65                  70                  75

agc ttt ctt cat aat atg aaa tat tta ggc tta atg tgg att ctc ggg     773
Ser Phe Leu His Asn Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly
                80                  85                  90

ata tcc atc atc ggt ctg ccc gtc att ttt atc atg gtc ttc tta aaa     821
Ile Ser Ile Ile Gly Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys
                95                  100                 105

ggg atc gtc gtc gga ttt aca gtc ggc ttt ttg gtc aat caa atg gga     869
Gly Ile Val Val Gly Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly
            110                 115                 120

atc aac ggc ttt ttc ctg tct ttt gtc tcc gtg ctc ccg caa aat att     917
Ile Asn Gly Phe Phe Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile
```

```
Ile Asn Gly Phe Phe Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile
125             130             135
```

```
ctg ctg atc ccg gcg tac ttg atc atg ggc acc tgc gcc atc gcc ttt    965
Leu Leu Ile Pro Ala Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe
140             145             150             155
```

```
tcg atg agg ctc atc cgc cag ctt ttt gta aac gca gcc ttc aga agc    1013
Ser Met Arg Leu Ile Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser
                160             165             170
```

```
acc tgt cca tgt gtt gtg ccg cgg gta gcc ga                         1045
Thr Cys Pro Cys Val Val Pro Arg Val Ala
            175             180
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<210> 69

<211> 181

<212> PRT

<213> Bacillus licheniformis

<400> 69

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Met Arg Lys Pro Thr Ile Lys Glu Leu Ile Phe Gln His Met Lys Asp
1               5               10              15
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His Leu Ser Ile Tyr Leu Phe Val Ser Val Leu Phe Leu Met Gly Val
                20              25              30
```

```
Ile Phe Gly Ala Val Ile Val Asn Ser Met Thr Ile Gly Gln Lys Glu
            35              40              45
```

```
Asp Leu Phe Tyr Tyr Leu Asn Gln Phe Phe Gly Gln Leu Ser Glu Gly
        50              55              60
```

```
Lys Ala Ala Ser Ser Lys Glu Met Phe Leu Gln Ser Phe Leu His Asn
65              70              75              80
```

```
Met Lys Tyr Leu Gly Leu Met Trp Ile Leu Gly Ile Ser Ile Ile Gly
                85              90              95
```

```
Leu Pro Val Ile Phe Ile Met Val Phe Leu Lys Gly Ile Val Val Gly
                100             105             110
```

```
Phe Thr Val Gly Phe Leu Val Asn Gln Met Gly Ile Asn Gly Phe Phe
                115             120             125
```

```
Leu Ser Phe Val Ser Val Leu Pro Gln Asn Ile Leu Leu Ile Pro Ala
            130             135             140
```

```
Tyr Leu Ile Met Gly Thr Cys Ala Ile Ala Phe Ser Met Arg Leu Ile
145             150             155             160
```

```
Arg Gln Leu Phe Val Asn Ala Ala Phe Arg Ser Thr Cys Pro Cys Val
            165                 170                 175

Val Pro Arg Val Ala
            180
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<210> 70

<211> 1108

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (500)..(1108)

<223>

<400> 70

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agtggtcgat gccgtcacga tcacgagcga cacgattgat tacatgctga agcatttgg      60

aagagagatg agagacgaca gtccgtccag gtcgctcgtt cccgcgggga tgagctttgg     120

gaaaagaaag gtcctcaccg aagaagacct tcccgatgaa gagcaccgca aatcgtttct     180

cggtatagtc ggaggcctcg cagaggatga aaaaaggcag ctgatccatg aagtcctcgc     240

tccgctcggc cataacttaa tggtgacccc taaagaggtc gatacattta tcgatgatat     300

ggcaaatgtg attgcaaacg gtctgaacac agcgctccat gaaaatgtat cgcaagacaa     360

taaaggaatg tataaccact aagatcaagg cggctggccc ggccgctttt tttcatgaca     420

tttagcattg ccggaacttg ttctacttcc tctatcttgt acatagtcta tttactagac     480

aagctctgga gggatttac aat gag aaa aag agg cag gaa tcg tca gtt tgt     532
                       Asn Glu Lys Lys Arg Gln Glu Ser Ser Val Cys
                        1               5                  10

gct ggc tgt aaa tgg aag aag cgc ggt tca gac agt att ctt att tat     580
Ala Gly Cys Lys Trp Lys Lys Arg Gly Ser Asp Ser Ile Leu Ile Tyr
            15                  20                  25

cgt cag cct gct gct cgt ttt tat ttt atc agg cgt gct cac atc gct     628
Arg Gln Pro Ala Ala Arg Phe Tyr Phe Ile Arg Arg Ala His Ile Ala
            30                  35                  40

gcg tcc tca gtt aag gcc gtc ttc atc gtt gta ccg ggt ggc tca tca     676
Ala Ser Ser Val Lys Ala Val Phe Ile Val Val Pro Gly Gly Ser Ser
            45                  50                  55

act gaa ggg cga gac ctt tgg gct cat ttt ggg aat gga aaa cca cta     724
Thr Glu Gly Arg Asp Leu Trp Ala His Phe Gly Asn Gly Lys Pro Leu
60                  65                  70                  75

ctt tgc atc aga att gcc gga acc gaa tca gcg ctt tca gct ttc ccc     772
Leu Cys Ile Arg Ile Ala Gly Thr Glu Ser Ala Leu Ser Ala Phe Pro
            80                  85                  90
```

```
cct cgt cct gaa gct ggc gac cag cat tca ttt gaa aga tcc gcg aag     820
Pro Arg Pro Glu Ala Gly Asp Gln His Ser Phe Glu Arg Ser Ala Lys
            95              100             105

ttt tct cgg acg gga gct tcc ggg att ctc tca ttt tca ctc gga aat     868
Phe Ser Arg Thr Gly Ala Ser Gly Ile Leu Ser Phe Ser Leu Gly Asn
            110             115             120

cct cat tgc cgg gca agg gac gga tta tac gaa tat gcc gtc aga atc     916
Pro His Cys Arg Ala Arg Asp Gly Leu Tyr Glu Tyr Ala Val Arg Ile
    125             130             135

tcc gcc gcc gac tca ggt ctt aaa aga gga gag aga agc gaa tct tgc     964
Ser Ala Ala Asp Ser Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys
140             145             150             155

aga gct tca agg gaa aca gaa aaa gaa aac aga cgg gga aaa acc tcc     1012
Arg Ala Ser Arg Glu Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser
            160             165             170

tca aca atc gac ggg cgg ccg caa agt cgt att tat cta caa tac gca     1060
Ser Thr Ile Asp Gly Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala
            175             180             185

caa tac gga atc gta tct tcc cct ttt aaa agg tca ggc aga tcc ttt     1108
Gln Tyr Gly Ile Val Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe
            190             195             200
```

<210> 71

<211> 203

<212> PRT

<213> Bacillus licheniformis

<400> 71

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Asn Glu Lys Lys Arg Gln Glu Ser Ser Val Cys Ala Gly Cys Lys Trp
1               5               10              15

Lys Lys Arg Gly Ser Asp Ser Ile Leu Ile Tyr Arg Gln Pro Ala Ala
            20              25              30

Arg Phe Tyr Phe Ile Arg Arg Ala His Ile Ala Ala Ser Ser Val Lys
        35              40              45

Ala Val Phe Ile Val Val Pro Gly Gly Ser Ser Thr Glu Gly Arg Asp
        50              55              60

Leu Trp Ala His Phe Gly Asn Gly Lys Pro Leu Leu Cys Ile Arg Ile
65              70              75              80

Ala Gly Thr Glu Ser Ala Leu Ser Ala Phe Pro Pro Arg Pro Glu Ala
            85              90              95

Gly Asp Gln His Ser Phe Glu Arg Ser Ala Lys Phe Ser Arg Thr Gly
            100             105             110
```

```
Ala Ser Gly Ile Leu Ser Phe Ser Leu Gly Asn Pro His Cys Arg Ala
        115                 120             125
```

```
Arg Asp Gly Leu Tyr Glu Tyr Ala Val Arg Ile Ser Ala Ala Asp Ser
    130                 135             140
```

```
Gly Leu Lys Arg Gly Glu Arg Ser Glu Ser Cys Arg Ala Ser Arg Glu
145             150             155             160
```

```
Thr Glu Lys Glu Asn Arg Arg Gly Lys Thr Ser Ser Thr Ile Asp Gly
                165             170             175
```

```
Arg Pro Gln Ser Arg Ile Tyr Leu Gln Tyr Ala Gln Tyr Gly Ile Val
            180             185             190
```

```
Ser Ser Pro Phe Lys Arg Ser Gly Arg Ser Phe
        195             200
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<210> 72

<211> 1152

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (107)..(985)

<223>

<400> 72
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ttgtttttaa ttaaaaacga aacaagctgg tgcaaaatta attgaaaaaa agttttttgg      60

taaaagtata aatttcatga agagggttca gaatggtgct gaggtg atg agt aag      115
                                                    Met Ser Lys
                                                     1
```

```
aaa gag aaa gag aag aat cgt act tcc aaa atc aca aag ttg caa caa      163
Lys Glu Lys Glu Lys Asn Arg Thr Ser Lys Ile Thr Lys Leu Gln Gln
     5                   10                  15
```

```
ttt ttt cgt aaa cgc tgg gta ttt ccg gcc atc tat ttg aca agt gcc      211
Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu Thr Ser Ala
20                  25                  30                  35
```

```
gtc gtt gta tta acc gcc gtt cta tgg tat caa tcg gct tct aac aac      259
Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala Ser Asn Asn
                40                  45                  50
```

```
gat gta aaa gac cag ctt gca gac gat ggc aag aaa tca gcc tat gat      307
Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser Ala Tyr Asp
            55                  60                  65
```

```
aac cgg gat gat gcg gta gaa gta ggc aaa cca gtc gaa aat gtc gca      355
Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu Asn Val Ala
        70                  75                  80

atg ccg gtt gct gat tct gaa aat gtt tcc gtc gtt aaa aag ttt ttt      403
Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys Lys Phe Phe
        85                  90                  95

gaa act gac gca act aaa gaa gag aaa gaa gca gca ctt gta aac tat      451
Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu Val Asn Tyr
100                 105                 110                 115

aat aac acg tac agc atg agc aaa ggt atc gac ttg gct gag aaa gac      499
Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala Glu Lys Asp
                    120                 125                 130

gga aaa aca ttt gat gtt tcc gca tct cta agc ggt acg gtc atc aaa      547
Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr Val Ile Lys
                135                 140                 145

gct gca aaa gac cct gta ctg ggc tac gtt gtt gaa gtt gaa cat gaa      595
Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val Glu His Glu
        150                 155                 160

gat ggt tta tca act gtg tat cag tct ctt tct gaa gta agc gtc aaa      643
Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val Ser Val Lys
        165                 170                 175

caa ggt gac aag att gaa caa aat caa gtc atc gga aaa gca ggc aaa      691
Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys Ala Gly Lys
180                 185                 190                 195

aac ctt tac aat gaa gaa ggc gga aac cat gtg cat ttt gaa atc cgc      739
Asn Leu Tyr Asn Glu Glu Gly Gly Asn His Val His Phe Glu Ile Arg
                    200                 205                 210

aaa gac ggt gtt gcg cta aac ccg ctg aac ttc atg gac aag ccg gtc      787
Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp Lys Pro Val
                215                 220                 225

tcc agc att gaa aaa gca atg gag gaa caa gcg tct gaa gtg aaa gaa      835
Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu Val Lys Glu
                230                 235                 240

cct gct cag cct tct gtt gaa gaa aag tca aaa aca gaa gac aaa gcg      883
Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu Asp Lys Ala
        245                 250                 255

aaa gat caa aca gat gga aaa gac gac aaa acc aag cgg gaa gat tcg      931
Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg Glu Asp Ser
260                 265                 270                 275

tct gaa ggg tca gaa aat caa gac gga acc cag tct gac gat tca agc      979
Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp Asp Ser Ser
                280                 285                 290

cag tca taaggcacgc ttccctcagg gcgcctatca aatgcgatag gcgccttttt     1035
Gln Ser

tgttacaatc aaaaaaaacc cgtatcaaat cggcggagcc agccgttttt aagtaagagg    1095

cctctttaag gagtggaagg cattaggaag taagtagaac agcaaaccgc ctagtaa      1152
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<210> 73

<211> 293

<212> PRT

<213> Bacillus licheniformis

<400> 73

Met Ser Lys Lys Glu Lys Glu Lys Asn Arg Thr Ser Lys Ile Thr Lys
1   5   10   15

Leu Gln Gln Phe Phe Arg Lys Arg Trp Val Phe Pro Ala Ile Tyr Leu
            20   25   30

Thr Ser Ala Val Val Val Leu Thr Ala Val Leu Trp Tyr Gln Ser Ala
            35   40   45

Ser Asn Asn Asp Val Lys Asp Gln Leu Ala Asp Asp Gly Lys Lys Ser
    50   55   60

Ala Tyr Asp Asn Arg Asp Asp Ala Val Glu Val Gly Lys Pro Val Glu
65   70   75   80

Asn Val Ala Met Pro Val Ala Asp Ser Glu Asn Val Ser Val Val Lys
                85   90   95

Lys Phe Phe Glu Thr Asp Ala Thr Lys Glu Glu Lys Glu Ala Ala Leu
            100   105   110

Val Asn Tyr Asn Asn Thr Tyr Ser Met Ser Lys Gly Ile Asp Leu Ala
            115   120   125

Glu Lys Asp Gly Lys Thr Phe Asp Val Ser Ala Ser Leu Ser Gly Thr
    130   135   140

Val Ile Lys Ala Ala Lys Asp Pro Val Leu Gly Tyr Val Val Glu Val
145   150   155   160

Glu His Glu Asp Gly Leu Ser Thr Val Tyr Gln Ser Leu Ser Glu Val
                165   170   175

Ser Val Lys Gln Gly Asp Lys Ile Glu Gln Asn Gln Val Ile Gly Lys
            180   185   190

Ala Gly Lys Asn Leu Tyr Asn Glu Glu Gly Gly Asn His Val His Phe
            195   200   205

Glu Ile Arg Lys Asp Gly Val Ala Leu Asn Pro Leu Asn Phe Met Asp
    210   215   220

Lys Pro Val Ser Ser Ile Glu Lys Ala Met Glu Glu Gln Ala Ser Glu
225   230   235   240

Val Lys Glu Pro Ala Gln Pro Ser Val Glu Glu Lys Ser Lys Thr Glu
              245   250   255

Asp Lys Ala Lys Asp Gln Thr Asp Gly Lys Asp Asp Lys Thr Lys Arg
              260   265   270

Glu Asp Ser Ser Glu Gly Ser Glu Asn Gln Asp Gly Thr Gln Ser Asp
          275   280   285

Asp Ser Ser Gln Ser
          290

<210> 74

<211> 1747

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1244)

<223>

<400> 74
gctttaatcg cgggtaactt gcacagtaca accgacatcc cgttctgggt gcagtttgca   60

tgcgccatgg ccatgggact cggaacatct gtcggcggct ggaaaatcat caaaaccgtc   120

ggcggaaaaa tcatgaagat ccgtcccgtc aacggtgtct ctgcagattt gacgggagcc   180

ctcatcatct ttggcgcgac gatcgtccat ttgcctgtca gcacgacaca cgtcatttct   240

tcatccattt taggcgtggg cgcttcccac cgggtgaaag gcgtaaactg gggcaccgca   300

aagcggatgc tgatcacttg ggtcattacc cttcccattt cggcaaccat cggtgcattt   360

gcctatttca tacttgattt attcttttaa tcagcacact cccgtccgaa tctaggacgg   420

gagttttcat gtttaaaaga aagccggcat aacaatagaa ataggaactg cactatttct   480

cggaagagg gaaacaagtt atg ctg cta ttt tat caa ttc ctt gtt tgg ctt   533
                        Met Leu Leu Phe Tyr Gln Phe Leu Val Trp Leu
                         1   5   10

att gtt ttg gcg ctg gct ctg tac gta gct gcc gtg tgg cgt ttt gaa   581
Ile Val Leu Ala Leu Ala Leu Tyr Val Ala Ala Val Trp Arg Phe Glu
              15   20   25

aaa cag ctc gcc gaa aaa acg gtc gcc atc aga aaa acg tgg tac ctt   629
Lys Gln Leu Ala Glu Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu
          30   35   40

ctt tat gtc atc ggc gcc gtg ata tat tgg acg cac gat ccg cag tca   677

Page 111

```
         Leu Tyr Val Ile Gly Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser
             45                  50                  55

         att ttc aca aac ccg ctt cat tac ctg atc gtt gcc gtt ttt ttc acg    725
         Ile Phe Thr Asn Pro Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr
         60                  65                  70                  75

         ttg aca gac gct ttt att ttc tta aat gcc tac ttt aaa aag ctc ggc    773
         Leu Thr Asp Ala Phe Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly
                             80                  85                  90

         agc tct gaa ctc gcg aca gat aca aga atg ctt ctc gaa gaa aac aac    821
         Ser Ser Glu Leu Ala Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn
                      95                 100                 105

         gac ctc ctc cac acg tat caa aac agg ctg aaa acg ttt caa tac cta    869
         Asp Leu Leu His Thr Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu
                     110                 115                 120

         ttg aaa aac gaa ccg atc cac atc tat tat gga aat ata gaa gcg tat    917
         Leu Lys Asn Glu Pro Ile His Ile Tyr Tyr Gly Asn Ile Glu Ala Tyr
             125                 130                 135

         gca gaa ggc atc gaa aag ctc atc aaa cgg ttt gcc gaa aaa atg aat    965
         Ala Glu Gly Ile Glu Lys Leu Ile Lys Arg Phe Ala Glu Lys Met Asn
         140                 145                 150                 155

         ata tcc gct gca ctt tgc gaa tat aat tca gaa gaa agc aag gat cat   1013
         Ile Ser Ala Ala Leu Cys Glu Tyr Asn Ser Glu Glu Ser Lys Asp His
                             160                 165                 170

         ttg ctt gag cat atg gaa aac cgg ttc gat gtt caa gaa aag ctt gac   1061
         Leu Leu Glu His Met Glu Asn Arg Phe Asp Val Gln Glu Lys Leu Asp
                     175                 180                 185

         cgc aaa gac gtt tat tat gaa gaa aac gga aaa atg gtc ctc att cct   1109
         Arg Lys Asp Val Tyr Tyr Glu Glu Asn Gly Lys Met Val Leu Ile Pro
                     190                 195                 200

         ttt tcc atc cac gat ttt gac tat gtc atg aag tta acc tca gaa gac   1157
         Phe Ser Ile His Asp Phe Asp Tyr Val Met Lys Leu Thr Ser Glu Asp
             205                 210                 215

         ctt gtc aca gaa ttt gat tat ctc ctg ttt act tct tta aca agc atc   1205
         Leu Val Thr Glu Phe Asp Tyr Leu Leu Phe Thr Ser Leu Thr Ser Ile
         220                 225                 230                 235

         tat gat ctt ctg cta cca aac gaa gag gaa ggt gac gac tgatggagcc   1254
         Tyr Asp Leu Leu Leu Pro Asn Glu Glu Glu Gly Asp Asp
                         240                 245

         tgcttttcag caagaccagg aaagcgtaaa aaagcgcctc gcctttaaaa tgtttaaaag   1314

         gcaatccaaa accaatatcg cgaaatacga agtcagcccc tataccgaac ggattttccg   1374

         gcaaaacgaa cggctgatcg gcgagtataa aagaaaaaaa gcttaacgag gacgggaaaa   1434

         aaattctccc gtccttattc cgttttcccg tttcttacat acaataaacc aatcaactaa   1494

         accgctgaat taggtgatgc tgtgaaaaaa ctgaaaaaac aagtcaaaca cgtcgatttc   1554

         gcaaaattcg gcctgtcaga ctatacctct cttctcagaa gaagaagcga aaaaatcatt   1614

         aaaacgctga acagaagaaa aaacaaaccg tgaagcttgg actttcaccc tccttctctg   1674

         ctgagaaggg gggttatttt catgtctaca ggagcatcat aaaggatgcc cctgtccgcc   1734

         ttctcctaca gat                                                    1747
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<210> 75

<211> 248

<212> PRT

<213> Bacillus licheniformis

<400> 75

Met Leu Leu Phe Tyr Gln Phe Leu Val Trp Leu Ile Val Leu Ala Leu
1   5   10   15

Ala Leu Tyr Val Ala Ala Val Trp Arg Phe Glu Lys Gln Leu Ala Glu
                20   25   30

Lys Thr Val Ala Ile Arg Lys Thr Trp Tyr Leu Leu Tyr Val Ile Gly
            35   40   45

Ala Val Ile Tyr Trp Thr His Asp Pro Gln Ser Ile Phe Thr Asn Pro
        50   55   60

Leu His Tyr Leu Ile Val Ala Val Phe Phe Thr Leu Thr Asp Ala Phe
65   70   75   80

Ile Phe Leu Asn Ala Tyr Phe Lys Lys Leu Gly Ser Ser Glu Leu Ala
                85   90   95

Thr Asp Thr Arg Met Leu Leu Glu Glu Asn Asn Asp Leu Leu His Thr
                100   105   110

Tyr Gln Asn Arg Leu Lys Thr Phe Gln Tyr Leu Leu Lys Asn Glu Pro
            115   120   125

Ile His Ile Tyr Tyr Gly Asn Ile Glu Ala Tyr Ala Glu Gly Ile Glu
        130   135   140

Lys Leu Ile Lys Arg Phe Ala Glu Lys Met Asn Ile Ser Ala Ala Leu
145   150   155   160

Cys Glu Tyr Asn Ser Glu Glu Ser Lys Asp His Leu Leu Glu His Met
                165   170   175

Glu Asn Arg Phe Asp Val Gln Glu Lys Leu Asp Arg Lys Asp Val Tyr
                180   185   190

Tyr Glu Glu Asn Gly Lys Met Val Leu Ile Pro Phe Ser Ile His Asp
            195   200   205

Phe Asp Tyr Val Met Lys Leu Thr Ser Glu Asp Leu Val Thr Glu Phe
210   215   220

Page 113

```
Asp Tyr Leu Leu Phe Thr Ser Leu Thr Ser Ile Tyr Asp Leu Leu Leu
225             230             235             240

Pro Asn Glu Glu Glu Gly Asp Asp
            245
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<210> 76

<211> 2020

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1742)

<223>

<400> 76

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agttgagtta gaggaattaa aaacgaagag aaaagaactt ataaattgga ggctaaaaga     120

tattatttca gaagagattt taaaagagga aatggaagat ttacgagagg aagaaaaatt     180

aataataact cgaattgaaa aattacagca cctcattaaa ctcagagata aaaccttttt     240

aaccaatatc atttcaactt cactacacga tctaaagaac tttttcaata ttatcgaaga     300

tgatgacaaa aaggaattac ttcgttctct cattgaagag attcacgtaa atccaggaaa     360

aactactaag gatagaacga tcaaagaagt gatttataag tttgatttaa aatatttgaa     420

atcaattgaa ctaagagaag gggaacatct tttctctttt ttgtgtttca tattataatt     480

acaaggaagg gaggattatt atg cac gaa ata aaa cgt gtc gca att tac tgt     533
                        Met His Glu Ile Lys Arg Val Ala Ile Tyr Cys
                        1               5                   10

aga gtt tct acc gaa gag cag gca acg gaa gga tac agc ata tct gcc     581
Arg Val Ser Thr Glu Glu Gln Ala Thr Glu Gly Tyr Ser Ile Ser Ala
            15              20                  25

caa tta caa act tta cgt caa tat act cag tta tat ggt tgg gag att     629
Gln Leu Gln Thr Leu Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile
        30              35                  40

gca gag gaa tat gta gat gag gga ata agt gga aag aac att agc ggt     677
Ala Glu Glu Tyr Val Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly
    45              50                  55

cgc cct gca atg caa aaa ctt att tca gat gtt gaa aag gat aaa ttt     725
Arg Pro Ala Met Gln Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe
60              65                  70                  75

caa gct gtt ctt gtt tgg aag atc tca cgc cta tca cga aat atg tta     773
Gln Ala Val Leu Val Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu
```

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Gln Ala Val Leu Val Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu
              80              85              90

gat act ctc act cta tta gac aaa ttc gaa gat tat gga gta aag ttc     821
Asp Thr Leu Thr Leu Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe
            95              100             105

atc tct tac tct gaa aac ttt gat aca ggc agt cca att ggt cgt tta     869
Ile Ser Tyr Ser Glu Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu
            110             115             120

gtt gtt caa cta atg gct tcc att gca gaa atg gag cgt aat acg tta     917
Val Val Gln Leu Met Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu
            125             130             135

tct gag aac gtt aag ctc gga atg aaa cag aga gca tta gaa ggt tca     965
Ser Glu Asn Val Lys Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser
140             145             150             155

tgg aat gga ggc gtt gta ttt ggc tac gat aca att gaa aaa gag ctt    1013
Trp Asn Gly Gly Val Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu
                160             165             170

gtg atc aac aaa aag gaa gct gag att gta caa caa atc tat caa cta    1061
Val Ile Asn Lys Lys Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu
                175             180             185

tat gcc aat ggt aaa ggc tta aag tca atc gca aac tac tta aat aaa    1109
Tyr Ala Asn Gly Lys Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys
            190             195             200

gca ggt tac aga act aaa cgg aat tgt tat ttt tcg ata aac ggt gta    1157
Ala Gly Tyr Arg Thr Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val
            205             210             215

gct caa atc tta gac aat gtt atc tat aac ggg aag atc agt tgg tta    1205
Ala Gln Ile Leu Asp Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu
220             225             230             235

aaa gtt gaa aat tgg gat aca aaa cgg agg aga ggg aaa aat cca aat    1253
Lys Val Glu Asn Trp Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn
                240             245             250

cct atc ctt gta gaa gga cag cat gaa gcc att att tcc gat gaa tta    1301
Pro Ile Leu Val Glu Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu
            255             260             265

tgg agt atg gta caa gca agg cgg aaa agt aaa tca ttt aaa caa agg    1349
Trp Ser Met Val Gln Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg
            270             275             280

caa tct aat gaa cca ttt tta ctt agc agt ctt tta cgt tgc ccc gat    1397
Gln Ser Asn Glu Pro Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp
            285             290             295

tgt ggt caa ggt atg gtt cct gcc att aca aca aat aaa cga aag gat    1445
Cys Gly Gln Gly Met Val Pro Ala Ile Thr Thr Asn Lys Arg Lys Asp
300             305             310             315

gga aca aag aag aaa tat cgt tat tat gtt tgc tct aac ttt cat aac    1493
Gly Thr Lys Lys Lys Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn
            320             325             330

aaa ggt tca tct gca tgt aga gca aat tca ata aaa gca tat gat gca    1541
Lys Gly Ser Ser Ala Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala
            335             340             345

gaa tac gaa gta att aat aag att gag aag atc ctt tcc aac caa aat    1589
```

Page 115

```
Glu Tyr Glu Val Ile Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn
        350             355             360

cag tta ttc tct aaa ctt caa tct ata aat act act tcg att gaa tct    1637
Gln Leu Phe Ser Lys Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser
        365             370             375

tta aac caa ctc aat agt gaa ttg aaa caa tta gaa aat cgc cta tca    1685
Leu Asn Gln Leu Asn Ser Glu Leu Lys Gln Leu Glu Asn Arg Leu Ser
380             385             390             395

gaa ata caa gag tac aga atc gtt act tgg aag cat ttg agc aaa aga    1733
Glu Ile Gln Glu Tyr Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg
                400             405             410

cct tac caa tagcaatctt gcaagaacga ttacagcatg tctctaaaga            1782
Pro Tyr Gln


aaaagcagag ttagaacaaa ggcacaatga atcactgggc aattaagctc gaacgatgca   1842

aaagtaataa aaccagaact gattcaaaag ctttagaaaa aattccttta gtctataaac   1902

atcatcaaga gaaagcaaaa cagttactca acttttgctt ataaattaca gtaagcatca   1962

atgggtcatc acgattgtcg atcaattgaa ctcgactttg actttcagaa gtcatatt     2020
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<210> 77

<211> 414

<212> PRT

<213> Bacillus licheniformis

<400> 77

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Met His Glu Ile Lys Arg Val Ala Ile Tyr Cys Arg Val Ser Thr Glu
1               5               10              15

Glu Gln Ala Thr Glu Gly Tyr Ser Ile Ser Ala Gln Leu Gln Thr Leu
            20              25              30

Arg Gln Tyr Thr Gln Leu Tyr Gly Trp Glu Ile Ala Glu Glu Tyr Val
        35              40              45

Asp Glu Gly Ile Ser Gly Lys Asn Ile Ser Gly Arg Pro Ala Met Gln
    50              55              60

Lys Leu Ile Ser Asp Val Glu Lys Asp Lys Phe Gln Ala Val Leu Val
65              70              75              80

Trp Lys Ile Ser Arg Leu Ser Arg Asn Met Leu Asp Thr Leu Thr Leu
                85              90              95

Leu Asp Lys Phe Glu Asp Tyr Gly Val Lys Phe Ile Ser Tyr Ser Glu
            100             105             110
```

Asn Phe Asp Thr Gly Ser Pro Ile Gly Arg Leu Val Val Gln Leu Met
        115   120   125

Ala Ser Ile Ala Glu Met Glu Arg Asn Thr Leu Ser Glu Asn Val Lys
        130   135   140

Leu Gly Met Lys Gln Arg Ala Leu Glu Gly Ser Trp Asn Gly Gly Val
145   150   155   160

Val Phe Gly Tyr Asp Thr Ile Glu Lys Glu Leu Val Ile Asn Lys Lys
            165   170   175

Glu Ala Glu Ile Val Gln Gln Ile Tyr Gln Leu Tyr Ala Asn Gly Lys
            180   185   190

Gly Leu Lys Ser Ile Ala Asn Tyr Leu Asn Lys Ala Gly Tyr Arg Thr
        195   200   205

Lys Arg Asn Cys Tyr Phe Ser Ile Asn Gly Val Ala Gln Ile Leu Asp
        210   215   220

Asn Val Ile Tyr Asn Gly Lys Ile Ser Trp Leu Lys Val Glu Asn Trp
225   230   235   240

Asp Thr Lys Arg Arg Arg Gly Lys Asn Pro Asn Pro Ile Leu Val Glu
            245   250   255

Gly Gln His Glu Ala Ile Ile Ser Asp Glu Leu Trp Ser Met Val Gln
            260   265   270

Ala Arg Arg Lys Ser Lys Ser Phe Lys Gln Arg Gln Ser Asn Glu Pro
        275   280   285

Phe Leu Leu Ser Ser Leu Leu Arg Cys Pro Asp Cys Gly Gln Gly Met
        290   295   300

Val Pro Ala Ile Thr Thr Asn Lys Arg Lys Asp Gly Thr Lys Lys Lys
305   310   315   320

Tyr Arg Tyr Tyr Val Cys Ser Asn Phe His Asn Lys Gly Ser Ser Ala
            325   330   335

Cys Arg Ala Asn Ser Ile Lys Ala Tyr Asp Ala Glu Tyr Glu Val Ile
        340   345   350

Asn Lys Ile Glu Lys Ile Leu Ser Asn Gln Asn Gln Leu Phe Ser Lys
        355   360   365

Leu Gln Ser Ile Asn Thr Thr Ser Ile Glu Ser Leu Asn Gln Leu Asn
370   375   380

Page 117

Ser Glu Leu Lys Gln Leu Glu Asn Arg Leu Ser Glu Ile Gln Glu Tyr
385   390   395   400

Arg Ile Val Thr Trp Lys His Leu Ser Lys Arg Pro Tyr Gln
              405   410

<210> 78

<211> 1417

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (510)..(1298)

<223>

<400> 78
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ctgaatgaat cagggtaaat tcggtttttt ctgcagaaag ctctttcaat tcaaatgtga   120

cgatccatcc cgacgtatcc cagctgaaag cgagtcgatg cggcgcatca agctcgatca   180

ctttgcacgg ggaggggccg aaaggagact gcagggtgaa ttcgcagccg atctccgggc   240

ggaaatcatt aggcataaac caggcggcga tgccttcact ggtggcgacg gcctcccaca   300

cttttttctat cgatgcgtga aaaacagcct gtttatgtat atcaggcact agttgattgc   360

tcataataga cctcctagaa aaagtaaaa ccaaatggtt tcctttctat tatatgaaac   420

cttttagttt tatgtcaatg ttccgtcata attccctggg acaaggcata tcattgaaca   480

aacgaacctg aatgtaaagg atgagggtt atg agt cat aga gca gat gag att   533
                                Met Ser His Arg Ala Asp Glu Ile
                                1   5

cga aaa aga atg gcc agg aaa aga aag cgg aaa aca ccg gac aaa cag   581
Arg Lys Arg Met Ala Arg Lys Arg Lys Arg Lys Thr Pro Asp Lys Gln
    10   15   20

ccc ttt tca tca gac ggc aaa aag cgg ccg ctc aag ccg cct gca tgg   629
Pro Phe Ser Ser Asp Gly Lys Lys Arg Pro Leu Lys Pro Pro Ala Trp
25   30   35   40

aca gcc ttt tcg gaa gat gaa aaa gga gga gac ttc cct ccg cct gaa   677
Thr Ala Phe Ser Glu Asp Glu Lys Gly Gly Asp Phe Pro Pro Pro Glu
                45   50   55

gga agt tcc ctg ctg ata aac ggg aag cac ccg ctt gtc aag gcg gat   725
Gly Ser Ser Leu Leu Ile Asn Gly Lys His Pro Leu Val Lys Ala Asp
                60   65   70

gcg ctc atc ttg aaa tgt ctt ctg tcg gca tgc ctt gtt ctt gtg tcc   773
Ala Leu Ile Leu Lys Cys Leu Leu Ser Ala Cys Leu Val Leu Val Ser
        75   80   85

Page 118

```
gcc att gcc tac aaa ggc cag ttt gaa ccc gca aac caa atc aaa ccg        821
Ala Ile Ala Tyr Lys Gly Gln Phe Glu Pro Ala Asn Gln Ile Lys Pro
    90              95              100

gtt atc agc cag gtg ttt act gaa gag ttc caa ttt gcg gcc ctc cag        869
Val Ile Ser Gln Val Phe Thr Glu Glu Phe Gln Phe Ala Ala Leu Gln
105             110             115             120

aat tgg tat gaa tcc aag ttc ggc gat ccc ctc gca ttc ttt cag ccg        917
Asn Trp Tyr Glu Ser Lys Phe Gly Asp Pro Leu Ala Phe Phe Gln Pro
                125             130             135

aaa ggc gcc aaa ccg tcc ggc cag gtc gag gtg aat cag gat ctc gct        965
Lys Gly Ala Lys Pro Ser Gly Gln Val Glu Val Asn Gln Asp Leu Ala
            140             145             150

gta cct gcc gta gga aag gtt cag gag aaa ttc tca ggg cag ggc att       1013
Val Pro Ala Val Gly Lys Val Gln Glu Lys Phe Ser Gly Gln Gly Ile
            155             160             165

aag gta gaa aca gaa gac gaa acg atc cgc agc atg aag gaa ggc tat       1061
Lys Val Glu Thr Glu Asp Glu Thr Ile Arg Ser Met Lys Glu Gly Tyr
    170             175             180

gtc att gaa gtg gac aaa aat ccg gaa aca ggc ctg acg gtg gtc ttg       1109
Val Ile Glu Val Asp Lys Asn Pro Glu Thr Gly Leu Thr Val Val Leu
105             190             195             200

cag cat gcg gac aac agc tat acc tac tac ggc cag ctg aaa aaa gcg       1157
Gln His Ala Asp Asn Ser Tyr Thr Tyr Tyr Gly Gln Leu Lys Lys Ala
                205             210             215

gat gtc gct tta tac gat tat ata gat aaa gga acg aag ctc gga acg       1205
Asp Val Ala Leu Tyr Asp Tyr Ile Asp Lys Gly Thr Lys Leu Gly Thr
            220             225             230

att gag cag gat aaa aat caa aaa ggc atc tat tac ttt gcg atc aaa       1253
Ile Glu Gln Asp Lys Asn Gln Lys Gly Ile Tyr Tyr Phe Ala Ile Lys
        235             240             245

caa gga gag gaa ttt gtt gat ccg ata cag gtg atc aca ttt gag           1298
Gln Gly Glu Glu Phe Val Asp Pro Ile Gln Val Ile Thr Phe Glu
    250             255             260

taaatggacg gagctcttca ccaagcttca cattcatccg ctgctgtggc ttgtcatggc     1358

gatcggtatc atgacaggac atattaaagg cgcgtgtttt gtttaatgca cccaggaag      1417
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<210> 79

<211> 263

<212> PRT

<213> Bacillus licheniformis

<400> 79

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Met Ser His Arg Ala Asp Glu Ile Arg Lys Arg Met Ala Arg Lys Arg
1               5               10              15


Lys Arg Lys Thr Pro Asp Lys Gln Pro Phe Ser Ser Asp Gly Lys Lys
            20              25              30
```

Arg Pro Leu Lys Pro Pro Ala Trp Thr Ala Phe Ser Glu Asp Glu Lys
        35   40   45

Gly Gly Asp Phe Pro Pro Pro Glu Gly Ser Ser Leu Leu Ile Asn Gly
        50   55   60

Lys His Pro Leu Val Lys Ala Asp Ala Leu Ile Leu Lys Cys Leu Leu
65   70   75   80

Ser Ala Cys Leu Val Leu Val Ser Ala Ile Ala Tyr Lys Gly Gln Phe
                85   90   95

Glu Pro Ala Asn Gln Ile Lys Pro Val Ile Ser Gln Val Phe Thr Glu
            100   105   110

Glu Phe Gln Phe Ala Ala Leu Gln Asn Trp Tyr Glu Ser Lys Phe Gly
        115   120   125

Asp Pro Leu Ala Phe Phe Gln Pro Lys Gly Ala Lys Pro Ser Gly Gln
    130   135   140

Val Glu Val Asn Gln Asp Leu Ala Val Pro Ala Val Gly Lys Val Gln
145   150   155   160

Glu Lys Phe Ser Gly Gln Gly Ile Lys Val Glu Thr Glu Asp Glu Thr
            165   170   175

Ile Arg Ser Met Lys Glu Gly Tyr Val Ile Glu Val Asp Lys Asn Pro
            180   185   190

Glu Thr Gly Leu Thr Val Val Leu Gln His Ala Asp Asn Ser Tyr Thr
        195   200   205

Tyr Tyr Gly Gln Leu Lys Lys Ala Asp Val Ala Leu Tyr Asp Tyr Ile
    210   215   220

Asp Lys Gly Thr Lys Leu Gly Thr Ile Glu Gln Asp Lys Asn Gln Lys
225   230   235   240

Gly Ile Tyr Tyr Phe Ala Ile Lys Gln Gly Glu Glu Phe Val Asp Pro
            245   250   255

Ile Gln Val Ile Thr Phe Glu
            260

<210>   80

<211>   1468

<212>   DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (982)..(1428)

<223>

<400> 80

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cggccatatc gcacaggtag cgggtgaccg cggatacaaa gaaaagcttg aacggctgcc      60

tatttatcag gtcagcaaag cggatcaaag catggtggtg ctggacgtga tgaaggtgat     120

tgaagctgta cataaatcgt ttcctgacct tgatgtccaa accgtcggcg gttctgaaac     180

catcgtggag atccaatatc cgaaaaggga tctgtcgccc gtgcttttca tcgccgtctg     240

gctgctcttg ttcgtcggtg ccggccttgc cgtcatgaac tttcatgaag atgtcagcat     300

gagggaagtg cacatcctgc tttacgaaat ggtgacgggc aaggtgaacc gctatccata     360

cctttttgcag gttccgtaca gcatcggtct tggcctcggc atgatcttgt tttttaatca     420

tttatttaaa aaacggttta acgaggagcc cagccccctg gaggtcgaga tgtttaaata     480

tcagcttgat ttggaccatt atgtggccat gcacgaaaac aaagaaacga caaaggatat     540

tcatgatcat tagcgtgata tttatcatct ttctcggact cgcaggaggg gttgctgttg     600

gatccggctt tgtcgctttt cttaccgtgc ttggcattat cccgaggctg actcagctga     660

cgaaaacaaa aggatttatc caggcgtatg aatgggctgt cattttaggc gcggttttcg     720

gaggatggga atcgctgaac atgtcccgct tttttttatc caaatggctg cttgttccga     780

tcggcctttt tgcgggcgtt ttcattggaa tgcttgcagc ggcgctaaca gaagtcttga     840

acgtgctgcc gatactggcg aaacgcatcg ggatgggaga ccggattttg atactttttaa     900

tggccattgt tttcggcaag attctcggat cgatgttcca atggctcatt tttgttcatt     960
```

```
tgtcataaaa ggaggattat g atg tca agt ttg aaa gat aat tat caa tcg     1011
                         Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser
                          1               5                  10

aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc     1059
Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile
             15              20                  25

aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc     1107
Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe
         30                  35                  40

cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg     1155
Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly
         45                  50                  55

aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc     1203
Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly
     60                  65                  70

ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc     1251
Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala
```

```
Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala
75              80              85              90

gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag    1299
Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu
                95              100             105

cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag    1347
His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys
            110             115             120

ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg    1395
Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val
            125             130             135

ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa  1448
Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe
        140             145

attaacagga aaacaaacat                                               1468
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<210> 81

<211> 149

<212> PRT

<213> Bacillus licheniformis

<400> 81

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Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser Lys Val Lys Ala Tyr Gln
1               5               10              15

Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile Lys Ala Phe Leu Val Gly
                20              25              30

Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala
            35              40              45

Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr
        50              55              60

Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg
65              70              75              80

Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe
                85              90              95

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr
                100             105             110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile
            115             120             125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala
            130             135             140
```

he Asp Lys Leu Phe
45

:210>   82

:211>   1453

:212>   DNA

:213>   Bacillus licheniformis

<220>

<221>   CDS

<222>   (504)..(950)

<223>

<400> 82
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tatcagcttg atttggacca ttatgtggcc atgcacgaaa acaaagaaac gacaaaggat      60

attcatgatc attagcgtga tatttatcat ctttctcgga ctcgcaggag gggttgctgt     120

tggatccggc tttgtcgctt ttcttaccgt gcttggcatt atcccgaggc tgactcagct     180

gacgaaaaca aaaggattta tccaggcgta tgaatgggct gtcattttag gcgcggtttt     240

cggaggatgg gaatcgctga acatgtcccg ctttttttta tccaaatggc tgcttgttcc     300

gatcggcctt tttgcgggcg ttttcattgg aatgcttgca gcggcgctaa cagaagtctt     360

gaacgtgctg ccgatactgg cgaaacgcat cgggatggga gaccggattt tgatactttt     420

aatggccatt gttttcggca agattctcgg atcgatgttc caatggctca ttttgttca     480
```

```
tttgtcataa aaggaggatt atg atg tca agt ttg aaa gat aat tat caa tcg      533
                        Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser
                         1               5                   10

aaa gtt aaa gcg tat cag cct tca ccg cct tat gtc ctg aac tgt atc        581
Lys Val Lys Ala Tyr Gln Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile
                15              20                  25

aag gca ttt ctc gtc ggt ggt ctg att tgt acg atc ggc cag gct ttc        629
Lys Ala Phe Leu Val Gly Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe
        30                  35                  40

cag aat ttt tat atg gct gtg ttc cat ttt gat gaa aaa acg gcc ggg        677
Gln Asn Phe Tyr Met Ala Val Phe His Phe Asp Glu Lys Thr Ala Gly
        45                  50                  55

aac ccg acg gtt gcc acg ctg atc ctg atc tcc gct ctg tta aca ggc        725
Asn Pro Thr Val Ala Thr Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly
    60                  65                  70

ctt ggc gtc tac gac aga atc gga cag ttt gcc ggc gct ggt tct gcc        773
Leu Gly Val Tyr Asp Arg Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala
75                  80                  85                  90

gtt ccg gtt aca ggg ttt gcc aac agt atg acg agc gca gcg ctg gag        821
Val Pro Val Thr Gly Phe Ala Asn Ser
```

Page 123

```
Val Pro Val Thr Gly Phe Ala Asn Ser Met Thr Ser Ala Ala Leu Glu
            95              100              105

cat aaa agc gaa agc tac gtc ctc ggc gta tgg aca aac atg ttc aag    869
His Lys Ser Glu Ser Tyr Val Leu Gly Val Trp Thr Asn Met Phe Lys
            110              115              120

ctt gcg gga aac gtc atc gtg ttc ggt gtt gtg gcc gct tat att gtg    917
Leu Ala Gly Asn Val Ile Val Phe Gly Val Val Ala Ala Tyr Ile Val
            125              130              135

ggg atg atc cgc ttt gcc ttt gac aag ctg ttt taggaggaaa acatcatgaa  970
Gly Met Ile Arg Phe Ala Phe Asp Lys Leu Phe
            140              145

attaacagga aaacaaacat gggaattcga gaacccgctg tttgttaact caagcggaac   1030

agcggtcggt cccaagaaa aagaaggtcc tcttggacac ttatttgaca aaagctatga    1090

tgaaatgcac tgcaaccaga aaaactggga aatggcagag cgcaagctga tggaggatgc    1150

ggttcagtcc gcgttatcaa aacaaaatct taaaaaggaa gacatcgata tctttttggc    1210

tggcgatctg ctcaaccaaa acgtgacagc caactatgtg gcgcggcatt tgaaaattcc    1270

ttttctctgc ttatttggag catgctcgac atcaatggaa tcgatcgcga tcagttcggc    1330

gttgattgac gggggtttcg caaagcgcgc cctagcggca accagcagcc ataatgctac    1390

ggcagaaagg cagttccgct acccgacgga atacggggggg caaaaaccgg gaaccgcgac    1450

ttc                                                                  1453
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<210> 83

<211> 149

<212> PRT

<213> Bacillus licheniformis

<400> 83

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Met Ser Ser Leu Lys Asp Asn Tyr Gln Ser Lys Val Lys Ala Tyr Gln
1               5              10              15


Pro Ser Pro Pro Tyr Val Leu Asn Cys Ile Lys Ala Phe Leu Val Gly
            20              25              30


Gly Leu Ile Cys Thr Ile Gly Gln Ala Phe Gln Asn Phe Tyr Met Ala
            35              40              45


Val Phe His Phe Asp Glu Lys Thr Ala Gly Asn Pro Thr Val Ala Thr
    50              55              60


Leu Ile Leu Ile Ser Ala Leu Leu Thr Gly Leu Gly Val Tyr Asp Arg
65              70              75              80


Ile Gly Gln Phe Ala Gly Ala Gly Ser Ala Val Pro Val Thr Gly Phe
            85              90              95
```

Ala Asn Ser Met Thr Ser Ala Ala Leu Glu His Lys Ser Glu Ser Tyr
            100   105   110

Val Leu Gly Val Trp Thr Asn Met Phe Lys Leu Ala Gly Asn Val Ile
            115   120   125

Val Phe Gly Val Val Ala Ala Tyr Ile Val Gly Met Ile Arg Phe Ala
            130   135   140

Phe Asp Lys Leu Phe
145

<210>   84

<211>   2020

<212>   DNA

<213>   Bacillus licheniformis

<220>

<221>   CDS

<222>   (501)..(1517)

<223>

<400>   84
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atcaatcgaa agttaaagcg tatcagcctt caccgcctta tgtcctgaac tgtatcaagg   120

catttctcgt cggtggtctg atttgtacga tcggccaggc tttccagaat ttttatatgg   180

ctgtgttcca ttttgatgaa aaaacggccg ggaacccgac ggttgccacg ctgatcctga   240

tctccgctct gttaacaggc cttggcgtct acgacagaat cggacagttt gccggcgctg   300

gttctgccgt tccggttaca gggtttgcca acagtatgac gagcgcagcg ctggagcata   360

aaagcgaaag ctacgtcctc ggcgtatgga caaacatgtt caagcttgcg ggaaacgtca   420

tcgtgttcgg tgttgtggcc gcttatattg tggggatgat ccgctttgcc tttgacaagc   480

tgtttttagga ggaaaacatc atg aaa tta aca gga aaa caa aca tgg gaa ttc   533
                          Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe
                           1   5   10

gag aac ccg ctg ttt gtt aac tca agc gga aca gcg gtc ggt ccc aaa   581
Glu Asn Pro Leu Phe Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys
                15   20   25

gaa aaa gaa ggt cct ctt gga cac tta ttt gac aaa agc tat gat gaa   629
Glu Lys Glu Gly Pro Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu
            30   35   40

atg cac tgc aac cag aaa aac tgg gaa atg gca gag cgc aag ctg atg   677

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            Met His Cys Asn Gln Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met
                45              50              55

gag gat gcg gtt cag tcc gcg tta tca aaa caa aat ctt aaa aag gaa       725
Glu Asp Ala Val Gln Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu
60              65              70              75

gac atc gat atc ttt ttg gct ggc gat ctg ctc aac caa aac gtg aca       773
Asp Ile Asp Ile Phe Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr
                80              85              90

gcc aac tat gtg gcg cgg cat ttg aaa att cct ttt ctc tgc tta ttt       821
Ala Asn Tyr Val Ala Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe
                95              100             105

gga gca tgc tcg aca tca atg gaa tcg atc gcg atc agt tcg gcg ttg       869
Gly Ala Cys Ser Thr Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu
            110             115             120

att gac ggg ggt ttc gca aag cgc gcc cta gcg gca acc agc agc cat       917
Ile Asp Gly Gly Phe Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His
        125             130             135

aat gct acg gca gaa agg cag ttc cgc tac ccg acg gaa tac ggg ggg       965
Asn Ala Thr Ala Glu Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly
140             145             150             155

caa aaa ccg gga acc gcg act tcg aca gtg acc gga agc gga gcg gtc      1013
Gln Lys Pro Gly Thr Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val
            160             165             170

gtc ctc agc cag cag ccc ggc gga att aaa att aca agc gca act gtc      1061
Val Leu Ser Gln Gln Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val
            175             180             185

gga agg gtt atc gac ttg ggg att acc gat tcg caa gat atg ggg tcg      1109
Gly Arg Val Ile Asp Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser
            190             195             200

gcg atg gca ccc gct gct gcg gat acg atc aag cag cat ttg gag gat      1157
Ala Met Ala Pro Ala Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp
    205             210             215

ctg gga cgc acc cct gat gat tac gat ctg atc tta acc ggc gac ctt      1205
Leu Gly Arg Thr Pro Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu
220             225             230             235

tca ggc gtc ggc agc ccg att ttg aag gat ctg tta aaa gag gaa gga      1253
Ser Gly Val Gly Ser Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly
            240             245             250

atc aat gtc ggg aca aaa cat aat gac tgc ggg ctg atg atc tat acg      1301
Ile Asn Val Gly Thr Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr
            255             260             265

cct gac cag caa gtt ttt gca ggt gga agc gga tgc gct tgt tcc gcg      1349
Pro Asp Gln Gln Val Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala
    270             275             280

gtc gtc acc ttt gcc cat att ttc aaa gaa att gaa gcg gga agg ctg      1397
Val Val Thr Phe Ala His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu
    285             290             295

aac aga gtg ctt gtt gtc gcg aca ggc gcc ctt tta agc ccg acg atc      1445
Asn Arg Val Leu Val Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile
300             305             310             315

atc cag caa aaa gaa tcg ata cca tgc att gcc cat ggc gtc gta ttt      1493
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Page 126

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Ile Gln Gln Lys Glu Ser Ile Pro Cys Ile Ala His Gly Val Val Phe
            320             325             330

gaa cgg gcc gaa agg ggg aac gct taagatggag tatgtcattg cttttattgc      1547
Glu Arg Ala Glu Arg Gly Asn Ala
            335

aggcgggctg atttgcgtca tcggacagct cttgcttgat atcttcaaaa tgacgccggc      1607

tcatgtcatg tcaacttttg tcgtatctgg agcgatcctt gacggattcg gcatttacga      1667

ccgttttatc gaatttgccg gtgccggggc tacagtcccg attgtcagct tcggccactc      1727

tcttttgcac ggcgcgatgc accaggctga gaaacatggc tttatcggaa tcggcatggg      1787

gatatttgaa ctgacatctg ccggtatatc tgccgctatc ttgttcgctt ttcttgttgc      1847

cgtgattttt aaaccgaaag gataaaggaa aatgccagca aaacgcaagg tcattttggt      1907

cacagacggc gatatatacg ctgcaaaagc aatcgaatat gcagcaagaa aaacgggtgg      1967

ccgctgcatt tcccaatcgg cggggaatcc gagcgttaaa acaggaccgg agc            2020
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<210> 85

<211> 339

<212> PRT

<213> Bacillus licheniformis

<400> 85

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Met Lys Leu Thr Gly Lys Gln Thr Trp Glu Phe Glu Asn Pro Leu Phe
1               5               10              15

Val Asn Ser Ser Gly Thr Ala Val Gly Pro Lys Glu Lys Glu Gly Pro
            20              25              30

Leu Gly His Leu Phe Asp Lys Ser Tyr Asp Glu Met His Cys Asn Gln
            35              40              45

Lys Asn Trp Glu Met Ala Glu Arg Lys Leu Met Glu Asp Ala Val Gln
    50              55              60

Ser Ala Leu Ser Lys Gln Asn Leu Lys Lys Glu Asp Ile Asp Ile Phe
65              70              75              80

Leu Ala Gly Asp Leu Leu Asn Gln Asn Val Thr Ala Asn Tyr Val Ala
            85              90              95

Arg His Leu Lys Ile Pro Phe Leu Cys Leu Phe Gly Ala Cys Ser Thr
            100             105             110

Ser Met Glu Ser Ile Ala Ile Ser Ser Ala Leu Ile Asp Gly Gly Phe
            115             120             125
```

Ala Lys Arg Ala Leu Ala Ala Thr Ser Ser His Asn Ala Thr Ala Glu
    130   135   140

Arg Gln Phe Arg Tyr Pro Thr Glu Tyr Gly Gly Gln Lys Pro Gly Thr
145   150   155   160

Ala Thr Ser Thr Val Thr Gly Ser Gly Ala Val Val Leu Ser Gln Gln
                165   170   175

Pro Gly Gly Ile Lys Ile Thr Ser Ala Thr Val Gly Arg Val Ile Asp
            180   185   190

Leu Gly Ile Thr Asp Ser Gln Asp Met Gly Ser Ala Met Ala Pro Ala
        195   200   205

Ala Ala Asp Thr Ile Lys Gln His Leu Glu Asp Leu Gly Arg Thr Pro
    210   215   220

Asp Asp Tyr Asp Leu Ile Leu Thr Gly Asp Leu Ser Gly Val Gly Ser
225   230   235   240

Pro Ile Leu Lys Asp Leu Leu Lys Glu Glu Gly Ile Asn Val Gly Thr
            245   250   255

Lys His Asn Asp Cys Gly Leu Met Ile Tyr Thr Pro Asp Gln Gln Val
            260   265   270

Phe Ala Gly Gly Ser Gly Cys Ala Cys Ser Ala Val Val Thr Phe Ala
        275   280   285

His Ile Phe Lys Glu Ile Glu Ala Gly Arg Leu Asn Arg Val Leu Val
    290   295   300

Val Ala Thr Gly Ala Leu Leu Ser Pro Thr Ile Ile Gln Gln Lys Glu
305   310   315   320

Ser Ile Pro Cys Ile Ala His Gly Val Val Phe Glu Arg Ala Glu Arg
            325   330   335

Gly Asn Ala

<210> 86

<211> 2473

<212> DNA

<213> Bacillus licheniformis

<220>

<221>   CDS

<222>   (501)..(1970)

<223>

<400>   86

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cgttaaaaca ggaccggagc ttgtaaccat gatcctgcaa acccctcatg atcctgtatt    120

cgtcatgttt gatgattccg gacttcaagg tgaaggcccg ggagagacag ctatgaaata    180

tgtagcgatg catcccgata tcgaggtgct cggagtcatc gccgtcgctt caaaaactca    240

ttatgcagag tggacgagag tcgatgtatc aatcgatgca gaaggcgaac tgacagagta    300

cggcgtcgat aaacacgggg tcaaagagtt cgatgtcaaa cgaatgaatg gtgatacagt    360

ctattgcctt gaccagctgg atgttccgat cattgtcgga atcggtgata tcggtaagat    420

gaacagaaaa gacgatgtgg aaaaaggttc gccgattaca atgaaagcgg tcgagctcat    480

tttagaaagg agcgggtatc atg agt gct caa aag caa gag aag acg aac gta    533
                      Met Ser Ala Gln Lys Gln Glu Lys Thr Asn Val
                       1               5                  10

ttc ctt gat cct tct aag aat gaa gcg tat ttc aag aag cgg gtc ggc    581
Phe Leu Asp Pro Ser Lys Asn Glu Ala Tyr Phe Lys Lys Arg Val Gly
              15              20                  25

atg gga gaa agc ttt gac ctt ggc gta cgg aag gtc ttt att ctc gga    629
Met Gly Glu Ser Phe Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly
          30              35                  40

cat gaa gtt cag ctt tat tat gtc aac gga ttg tgc gac aca caa tac    677
His Glu Val Gln Leu Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr
     45              50                  55

atc att cac ctg tta aga gaa ctg gtg cat ctg aat gat aaa gaa aaa    725
Ile Ile His Leu Leu Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys
60              65                  70                  75

gaa tcg ggc gag gtc gaa gac atc gtc gaa aac agg ctt ttg aac cag    773
Glu Ser Gly Glu Val Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln
              80                  85                  90

cag gtt tca aaa gcg gaa acg ctt gat gaa gct gtc gac caa gtg ttg    821
Gln Val Ser Lys Ala Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu
          95                  100                 105

tca gga ctg gtt gcc atc atc gtc gaa gat gcg ggc ttt gct ttt atc    869
Ser Gly Leu Val Ala Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile
          110                 115                 120

atc gat gtc aga agc tac ccg ggc aga acg ccg gaa gaa cct gat aca    917
Ile Asp Val Arg Ser Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr
125                 130                 135

gaa aaa gtc gta cgc ggt gca agg gac gga ctc gtc gag aac atc atc    965
Glu Lys Val Val Arg Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile
140                 145                 150                 155

gtc aac aca gcc ctg att aga cgc cgg atc aga gat gag cgc ttg cgc   1013
Val Asn Thr Ala Leu Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg
              160                 165                 170
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tac aaa atg ctt cat atc ggt gaa cgc tct aaa aca gac atc tgc ctc        1061
Tyr Lys Met Leu His Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu
            175                 180                 185

tgc tat ttg gaa gac gtt gca gat ccc gat ctt gtt gaa gta tta aaa        1109
Cys Tyr Leu Glu Asp Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys
            190                 195                 200

aaa gaa att gaa gat gtg aag atc gac ggg ctg ccg atg tcg gat aaa        1157
Lys Glu Ile Glu Asp Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys
        205                 210                 215

tcg gta gag gaa ttc ctg gtc ggc caa ggc tac aat ccg ttt ccg ctt        1205
Ser Val Glu Glu Phe Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu
220                 225                 230                 235

gtc agg ttt acg gaa agg gca gac gta gcc gca agc cat att tta gag        1253
Val Arg Phe Thr Glu Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu
                240                 245                 250

ggg cat gtc atc gtg atc gtc gat acg tcg cca agc gtc atc atc aca        1301
Gly His Val Ile Val Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr
            255                 260                 265

ccg acc act ttg ttt cac cat gtt cag cat gct gag gaa tac aga cag        1349
Pro Thr Thr Leu Phe His His Val Gln His Ala Glu Glu Tyr Arg Gln
            270                 275                 280

acg ccg gct gtt ggg acg ttt tta agg tgg gtg cgg ttt ttc ggt att        1397
Thr Pro Ala Val Gly Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile
        285                 290                 295

ttg gcc tcc acc ttt ttg ctg ccg ctt tgg ctg ctg ttt gtc att cat        1445
Leu Ala Ser Thr Phe Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His
300                 305                 310                 315

ccg tcg ctc ttg cct gat aat tta tcg ttt atc ggg ttg aat aaa gac        1493
Pro Ser Leu Leu Pro Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp
                320                 325                 330

acc cat att ccg att atc atg cag att ttc ctg gcg gat ctc ggc gtc        1541
Thr His Ile Pro Ile Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val
                335                 340                 345

gaa ttt tta aga atg gcc gcc att cat acg ccg acg gcg ctt tcg act        1589
Glu Phe Leu Arg Met Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr
        350                 355                 360

gca atg ggc ctg atc gcc gct gta ttg atc ggc gat atc gcg atc aat        1637
Ala Met Gly Leu Ile Ala Ala Val Leu Ile Gly Asp Ile Ala Ile Asn
365                 370                 375

gtc ggc ttg ttt tct ccc gaa gtc att tta tac gtt tcc ctc tcg gca        1685
Val Gly Leu Phe Ser Pro Glu Val Ile Leu Tyr Val Ser Leu Ser Ala
380                 385                 390                 395

atc gga gcc tac acg aca cca agc tac gag ctg agc ctg gcg aat aaa        1733
Ile Gly Ala Tyr Thr Thr Pro Ser Tyr Glu Leu Ser Leu Ala Asn Lys
                400                 405                 410

atg gtg aag ctg ttt atg ctg ata ttg gtg gcg ctt ttt aaa gtg gag        1781
Met Val Lys Leu Phe Met Leu Ile Leu Val Ala Leu Phe Lys Val Glu
                415                 420                 425

gga ttt gtc atc gga tta acg atc tta act ata gtg atg act tcg atc        1829
Gly Phe Val Ile Gly Leu Thr Ile Leu Thr Ile Val Met Thr Ser Ile
            430                 435                 440
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Page 130

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agg tca ttg cga acg cct tac tta tgg cct ctc ctc ccg ttc aat gga      1877
Arg Ser Leu Arg Thr Pro Tyr Leu Trp Pro Leu Leu Pro Phe Asn Gly
    445                 450                 455

aaa gcg ttt tgg cat gtt ctc gtg cgc acg tcc gtt cca ggg gga aaa      1925
Lys Ala Phe Trp His Val Leu Val Arg Thr Ser Val Pro Gly Gly Lys
460                 465                 470                 475

gtc agg ccg agc atc gtt cat ccg aga aac cgc tcc aga cag ccg          1970
Val Arg Pro Ser Ile Val His Pro Arg Asn Arg Ser Arg Gln Pro
                480                 485                 490

tgaagccggc attcgaagag gcttttcccc ggggaaaagc ctcttttca ataatcgaat     2030

tccggtcttt gagtaccgat gcctctgtat tcattggcag agatcgcgac tgcccggagg    2090

ctgcagatgt tgttctgtct tctgatcgga tagacgacat acagcatttc gcggccgtac    2150

gggtcaatcg ttgacgaatg aaggaaaacc tcagttcctc tccgccaaaa tctcgtattc    2210

gccggagctg taataatctg cccttcataa ggctcataaa ttctctgttc ataatgcgca    2270

gccggctgat aaggggcgta tacatcttca ggtgcatagc cgggagcggg ggtgtaggga    2330

taacgatttg gatacatatg ataacctctt tcccacttcg ttttttggtt ttcatcttta    2390

agattatatt caggtaaatg cctatttgta tgggcgaaaa tctcagcttt tcggctcttt    2450

ttttattgaa tggacgttgt gta                                            2473
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<210> 87

<211> 490

<212> PRT

<213> Bacillus licheniformis

<400> 87

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Met Ser Ala Gln Lys Gln Glu Lys Thr Asn Val Phe Leu Asp Pro Ser
1               5                  10                  15


Lys Asn Glu Ala Tyr Phe Lys Lys Arg Val Gly Met Gly Glu Ser Phe
            20                  25                  30


Asp Leu Gly Val Arg Lys Val Phe Ile Leu Gly His Glu Val Gln Leu
        35                  40                  45


Tyr Tyr Val Asn Gly Leu Cys Asp Thr Gln Tyr Ile Ile His Leu Leu
    50                  55                  60


Arg Glu Leu Val His Leu Asn Asp Lys Glu Lys Glu Ser Gly Glu Val
65                  70                  75                  80


Glu Asp Ile Val Glu Asn Arg Leu Leu Asn Gln Gln Val Ser Lys Ala
                85                  90                  95
```

Glu Thr Leu Asp Glu Ala Val Asp Gln Val Leu Ser Gly Leu Val Ala
                100   105   110

Ile Ile Val Glu Asp Ala Gly Phe Ala Phe Ile Ile Asp Val Arg Ser
        115   120   125

Tyr Pro Gly Arg Thr Pro Glu Glu Pro Asp Thr Glu Lys Val Val Arg
    130   135   140

Gly Ala Arg Asp Gly Leu Val Glu Asn Ile Ile Val Asn Thr Ala Leu
145   150   155   160

Ile Arg Arg Arg Ile Arg Asp Glu Arg Leu Arg Tyr Lys Met Leu His
                165   170   175

Ile Gly Glu Arg Ser Lys Thr Asp Ile Cys Leu Cys Tyr Leu Glu Asp
            180   185   190

Val Ala Asp Pro Asp Leu Val Glu Val Leu Lys Lys Glu Ile Glu Asp
        195   200   205

Val Lys Ile Asp Gly Leu Pro Met Ser Asp Lys Ser Val Glu Glu Phe
    210   215   220

Leu Val Gly Gln Gly Tyr Asn Pro Phe Pro Leu Val Arg Phe Thr Glu
225   230   235   240

Arg Ala Asp Val Ala Ala Ser His Ile Leu Glu Gly His Val Ile Val
            245   250   255

Ile Val Asp Thr Ser Pro Ser Val Ile Ile Thr Pro Thr Thr Leu Phe
            260   265   270

His His Val Gln His Ala Glu Glu Tyr Arg Gln Thr Pro Ala Val Gly
        275   280   285

Thr Phe Leu Arg Trp Val Arg Phe Phe Gly Ile Leu Ala Ser Thr Phe
    290   295   300

Leu Leu Pro Leu Trp Leu Leu Phe Val Ile His Pro Ser Leu Leu Pro
305   310   315   320

Asp Asn Leu Ser Phe Ile Gly Leu Asn Lys Asp Thr His Ile Pro Ile
            325   330   335

Ile Met Gln Ile Phe Leu Ala Asp Leu Gly Val Glu Phe Leu Arg Met
            340   345   350

Ala Ala Ile His Thr Pro Thr Ala Leu Ser Thr Ala Met Gly Leu Ile
        355   360   365

Page 132

```
Ala Ala Val Leu Ile Gly Asp Ile Ala Ile Asn Val Gly Leu Phe Ser
    370             375             380

Pro Glu Val Ile Leu Tyr Val Ser Leu Ser Ala Ile Gly Ala Tyr Thr
385             390             395             400

Thr Pro Ser Tyr Glu Leu Ser Leu Ala Asn Lys Met Val Lys Leu Phe
            405             410             415

Met Leu Ile Leu Val Ala Leu Phe Lys Val Glu Gly Phe Val Ile Gly
            420             425             430

Leu Thr Ile Leu Thr Ile Val Met Thr Ser Ile Arg Ser Leu Arg Thr
        435             440             445

Pro Tyr Leu Trp Pro Leu Leu Pro Phe Asn Gly Lys Ala Phe Trp His
    450             455             460

Val Leu Val Arg Thr Ser Val Pro Gly Gly Lys Val Arg Pro Ser Ile
465             470             475             480

Val His Pro Arg Asn Arg Ser Arg Gln Pro
                485             490
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<210> 88

<211> 1567

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1064)

<223>

<400> 88
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cagccgcttt acgagctgtc tgtcacagca aagccgaaga acattccgca gacgatcgag     180
gttgatattt ccagtctcga agtcaatgat gttctaaccg tcggcgatat tccgaccaaa     240
ggcgattatt catacaacca tgagcctgat gaagttgttg catccattct tcctcctcaa     300
aagcaggaag aaacagaagc cgaatcagct gctcaagacg ttgaggaacc agaaaaaggc     360
actgaagagg aaaaagaaga ataaatacgt aagacgtaat ccgcccgcgg ttacgtcttt     420
tgtgctagaa tgaggggaaa ttaggatgct ccccctcagt atgctgaggc agggttttgc     480
```

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:taagggagg atatagaata atg ctt gtg ttt gca gga ttg ggc aat ccg ggt    533
                      Met Leu Val Phe Ala Gly Leu Gly Asn Pro Gly
                       1               5                  10

iaa aca tat gaa aat acg aga cac aat gta ggt ttt atg acg att gac      581
-ys Thr Tyr Glu Asn Thr Arg His Asn Val Gly Phe Met Thr Ile Asp
        15                  20                  25

jag ctc tcg aaa gag tgg aac att ccg ctt gat aaa aca aag ttc aac      629
5lu Leu Ser Lys Glu Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn
        30                  35                  40

gga caa tac gga atc ggg ttt gtt tcc ggc aaa aag gtt cta ctt gtt      677
Gly Gln Tyr Gly Ile Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val
    45                  50                  55

aag ccg ctt aca tat atg aat tta tcg gga gaa tgt ttg agg ccg ctt      725
Lys Pro Leu Thr Tyr Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu
60          65                  70                  75

ttg gac tat tac gag atc cct gtt gac aat ttg aaa gtg att tac gat      773
Leu Asp Tyr Tyr Glu Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp
                80                  85                  90

gat ttg gat ctt ccg acc gga aga atc cgt ctg agg acg aaa gga agc      821
Asp Leu Asp Leu Pro Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser
            95                  100                 105

gca gga ggc cat aac ggc atc aaa tcg acg att cag cat ctg gga aca      869
Ala Gly Gly His Asn Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr
        110                 115                 120

agt gag ttt aac cgg atc aga atc gga ata ggc cgt ccg gta aac ggc      917
Ser Glu Phe Asn Arg Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly
125                 130                 135

atg aaa gtc gtc gat tat gtg ctt ggc gct ttt aca gat gaa gaa gag     965
Met Lys Val Val Asp Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu
140                 145                 150                 155

ccg gcg ata aaa gag gcc gtc aga caa tcg gcc aag gcc tgt gaa gct    1013
Pro Ala Ile Lys Glu Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala
                160                 165                 170

tct ttg gaa aaa cct ttt tta gaa gtc atg aat gaa ttt aac gca aag    1061
Ser Leu Glu Lys Pro Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys
            175                 180                 185

gta taaggcaaaa gggaacggaa catactagtc ttaaaaagac tcggtatgga         1114
Val
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ggttccttta tggctttaca ttattattgc cggcattgcg gcgttaaagt cggaagtctt   1174
gaccattctt atgtaaacag tgaacagtta ggctttaacc acttaacaaa tgatgaaaga   1234
aacgatatga tttcttatat ggataatggg gatttacacg tgaagacgat atgtgaagat   1294
tgtcaagaag cgcttgagcg aaacccggat tatcaccaat atcattcatt tattcaatag   1354
atagctttgg tgtagagact agaccaaagc atttttctat ttgaggaaga gaggaggggc   1414
tcatttgaac aatattcaat cctatataac aaaaagcgat gattttaaat ccatcgtcaa   1474
cggcttgaac gaagggctga aggaacagct gcttgcgggg ctctccggat ctgcccggtc   1534
                                                                     1567
gttatttaca gccgctctta caaaagaaac gag
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Page 134

<210> 89

<211> 188

<212> PRT

<213> Bacillus licheniformis

<400> 89

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Met Leu Val Phe Ala Gly Leu Gly Asn Pro Gly Lys Thr Tyr Glu Asn
1               5                   10                  15

Thr Arg His Asn Val Gly Phe Met Thr Ile Asp Glu Leu Ser Lys Glu
                20              25                  30

Trp Asn Ile Pro Leu Asp Lys Thr Lys Phe Asn Gly Gln Tyr Gly Ile
            35                  40                  45

Gly Phe Val Ser Gly Lys Lys Val Leu Leu Val Lys Pro Leu Thr Tyr
        50                  55                  60

Met Asn Leu Ser Gly Glu Cys Leu Arg Pro Leu Leu Asp Tyr Tyr Glu
65                  70                  75                  80

Ile Pro Val Asp Asn Leu Lys Val Ile Tyr Asp Asp Leu Asp Leu Pro
                85                  90                  95

Thr Gly Arg Ile Arg Leu Arg Thr Lys Gly Ser Ala Gly Gly His Asn
                100                 105                 110

Gly Ile Lys Ser Thr Ile Gln His Leu Gly Thr Ser Glu Phe Asn Arg
            115                 120                 125

Ile Arg Ile Gly Ile Gly Arg Pro Val Asn Gly Met Lys Val Val Asp
        130                 135                 140

Tyr Val Leu Gly Ala Phe Thr Asp Glu Glu Glu Pro Ala Ile Lys Glu
145                 150                 155                 160

Ala Val Arg Gln Ser Ala Lys Ala Cys Glu Ala Ser Leu Glu Lys Pro
                165                 170                 175

Phe Leu Glu Val Met Asn Glu Phe Asn Ala Lys Val
                180             185
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<210> 90

<211> 2097

<212> DNA

213> Bacillus licheniformis

220>

221> CDS

222> (501)..(1598)

223>

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400>  90
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aacagactg ttttacaatg acagcaaagc gacaaacatt cttgcgacga aaaaagcgct     120

gtccgccttt caaaagccgg tcattttgct ggcagggggg cttgaccgcg gaaatgaatt    180

tgatgaacta aagccgcata tgtcttttgt aaaagcggtg atcactttcg gcgagaccgc    240

gccgaagttt gagaagctgg ccgaagaaat gggaatacaa caggttaaac gtgtcgataa    300

tgttgaacaa gcagcaactg cggcgttcag cctgtcagac gaaggagatg tcattcttct    360

gtccccggcc tgcgcaagct gggatcagta caaaacattt gaagaacgtg gtgacatgtt    420

tgtaaacgcc gtgcatatgc ttaaataagg gcttgtctcg taaagatagc cctaagaatt    480

agagcttggg gtgttcggct ttg caa aca aaa aaa acg tca ccg gat ttt ttg    533
                        Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu
                         1               5                  10

ctg gtt atc att acg cta ttg ctt tta aca atc gga ctg att atg gta    581
Leu Val Ile Ile Thr Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val
             15                  20                  25

tac agc gcc agt gca gta tgg gcg act tac aaa tac gac gac tcc ttt    629
Tyr Ser Ala Ser Ala Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe
         30                  35                  40

ttc ttt gcg aaa cgg cag ctt ttg ttt gcc ggc atc ggg gtc atc gcc    677
Phe Phe Ala Lys Arg Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala
     45                  50                  55

atg ttt ttc atc atg aac gtc gac tac tgg acg tgg agg act tat gcg    725
Met Phe Phe Ile Met Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala
60                  65                  70                  75

aaa ata ctg atc att gta tgt ttc ttt ctg ctc atc atc gtc ctg gtt    773
Lys Ile Leu Ile Ile Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val
                 80                  85                  90

ccc ggg atc ggc atg gaa cgg aac ggg tcg agg agc tgg atc gga gtc    821
Pro Gly Ile Gly Met Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val
             95                  100                 105

ggc gct ttc agc att cag ccg tcc gag ttt atg aaa ctc gcg atg atc    869
Gly Ala Phe Ser Ile Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile
         110                 115                 120

gca ttt ttg gcc aag ttt tta tct gaa aag caa aag aat att acg tcg    917
Ala Phe Leu Ala Lys Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser
     125                 130                 135

ttt aga aaa ggc ttt gtg ccg gcg ctg ggc att gtc ttt tca gct ttt    965
```

Page 136

```
Phe Arg Lys Gly Phe Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe
140             145             150             155

ctg atc atc atg atg cag cct gac ctc gga aca gga acc gtg atg gtc    1013
Leu Ile Ile Met Met Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val
            160             165             170

ggc aca tgc atc att atg atc ttt gtc gcg ggg gcg aga att tcg cac    1061
Gly Thr Cys Ile Ile Met Ile Phe Val Ala Gly Ala Arg Ile Ser His
            175             180             185

ttc gtt ttt ctc ggc ctg atc gga ctg agc ggt ttt gtc ggc ctt gtg    1109
Phe Val Phe Leu Gly Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val
            190             195             200

ctg tcg gcg ccg tac cgg atc aaa agg atc act tca tac ttg aac cct    1157
Leu Ser Ala Pro Tyr Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro
            205             210             215

tgg gag gac cct tta gga agc ggc ttt caa atc att cag tct ctt tat    1205
Trp Glu Asp Pro Leu Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr
220             225             230             235

gcg gtg ggg ccc ggc ggg ctg ttc ggc ctc ggc ctc ggc cag agc agg    1253
Ala Val Gly Pro Gly Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg
            240             245             250

caa aag ttt ttc tat ctg cct gag ccg cag aca gat ttt att ttt gcg    1301
Gln Lys Phe Phe Tyr Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala
            255             260             265

att tta tca gag gag ctc ggc ttt atc ggc gga tcg ctg att ctt ttg    1349
Ile Leu Ser Glu Glu Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu
            270             275             280

ctc ttc agc gtt cta tta tgg aga ggc atc aga atc gcg ctc ggt gcg    1397
Leu Phe Ser Val Leu Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala
    285             290             295

ccc gat tta tac ggc agt ttt gtc gcc gtc ggc gtc att tcg atg ata    1445
Pro Asp Leu Tyr Gly Ser Phe Val Ala Val Gly Val Ile Ser Met Ile
300             305             310             315

gcg att cag gtt atg atc aat atc gga gtc gtg act ggt ttg att cct    1493
Ala Ile Gln Val Met Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro
            320             325             330

gtt aca ggc att acg ctt ccg ttt tta agc tat ggc ggt tca tca ctg    1541
Val Thr Gly Ile Thr Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu
            335             340             345

acc ttg atg ctc atg gcg gtc ggc gtg ctg ctg aat gtc agc agg tat    1589
Thr Leu Met Leu Met Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr
            350             355             360

tct aga tac tagattttgg cgataaccct gttgcgagat agcagggtta            1638
Ser Arg Tyr
            365

tcggcgtgta cataaggatt aaggggggaga acagatgcgg attgttgtta gcggaggcgg    1698

aacgggcggc catatttacc ccgcccttgc gtttattaaa gaagtgaaac ggcatcacga    1758

agatgttgag tttttatata tcggaaccga aaaaggcctg gagaaaaata tcgtcgagcg    1818

ggaagggatc cctttcaaag cgattgaaat tacgggtttt aaaagaaaac tttcatttga    1878

aaacgtcaaa accgtcatgc gcttttttaaa gggtgtaaaa gaatgcaaag aagaattaaa    1938
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Page 137

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acggttcaag ccggatgccg tgatcggcac gggcggctac gtgtgcggcc ccgtcgtata    1998

cgccgcttca aaactgggga ttccgacgat tatccacgaa caaaacagcc ttcccggact    2058

caccaataag tttttatcca aatatgttga taaggtagc                           2097
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<210> 91

<211> 366

<212> PRT

<213> Bacillus licheniformis

<400> 91

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Leu Gln Thr Lys Lys Thr Ser Pro Asp Phe Leu Leu Val Ile Ile Thr
1               5                   10                  15

Leu Leu Leu Leu Thr Ile Gly Leu Ile Met Val Tyr Ser Ala Ser Ala
                20                  25                  30

Val Trp Ala Thr Tyr Lys Tyr Asp Asp Ser Phe Phe Phe Ala Lys Arg
            35                  40                  45

Gln Leu Leu Phe Ala Gly Ile Gly Val Ile Ala Met Phe Phe Ile Met
        50                  55                  60

Asn Val Asp Tyr Trp Thr Trp Arg Thr Tyr Ala Lys Ile Leu Ile Ile
65                  70                  75                  80

Val Cys Phe Phe Leu Leu Ile Ile Val Leu Val Pro Gly Ile Gly Met
                85                  90                  95

Glu Arg Asn Gly Ser Arg Ser Trp Ile Gly Val Gly Ala Phe Ser Ile
                100                 105                 110

Gln Pro Ser Glu Phe Met Lys Leu Ala Met Ile Ala Phe Leu Ala Lys
            115                 120                 125

Phe Leu Ser Glu Lys Gln Lys Asn Ile Thr Ser Phe Arg Lys Gly Phe
        130                 135                 140

Val Pro Ala Leu Gly Ile Val Phe Ser Ala Phe Leu Ile Ile Met Met
145                 150                 155                 160

Gln Pro Asp Leu Gly Thr Gly Thr Val Met Val Gly Thr Cys Ile Ile
                165                 170                 175

Met Ile Phe Val Ala Gly Ala Arg Ile Ser His Phe Val Phe Leu Gly
                180                 185                 190
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Leu Ile Gly Leu Ser Gly Phe Val Gly Leu Val Leu Ser Ala Pro Tyr
        195             200             205

Arg Ile Lys Arg Ile Thr Ser Tyr Leu Asn Pro Trp Glu Asp Pro Leu
    210             215             220

Gly Ser Gly Phe Gln Ile Ile Gln Ser Leu Tyr Ala Val Gly Pro Gly
225             230             235             240

Gly Leu Phe Gly Leu Gly Leu Gly Gln Ser Arg Gln Lys Phe Phe Tyr
            245             250             255

Leu Pro Glu Pro Gln Thr Asp Phe Ile Phe Ala Ile Leu Ser Glu Glu
            260             265             270

Leu Gly Phe Ile Gly Gly Ser Leu Ile Leu Leu Leu Phe Ser Val Leu
        275             280             285

Leu Trp Arg Gly Ile Arg Ile Ala Leu Gly Ala Pro Asp Leu Tyr Gly
    290             295             300

Ser Phe Val Ala Val Gly Val Ile Ser Met Ile Ala Ile Gln Val Met
305             310             315             320

Ile Asn Ile Gly Val Val Thr Gly Leu Ile Pro Val Thr Gly Ile Thr
            325             330             335

Leu Pro Phe Leu Ser Tyr Gly Gly Ser Ser Leu Thr Leu Met Leu Met
            340             345             350

Ala Val Gly Val Leu Leu Asn Val Ser Arg Tyr Ser Arg Tyr
        355             360             365
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<210> 92

<211> 1882

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1397)

<223>

<400> 92

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ctgccgaaat aatgcctcct taaaacatgc ttgtcttttt aggcaggcat gttttttgtt    60
atcggttcat acatcataac aaaaggggggt ttttttcatg aggctgagtg aactttcggg   120
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aaaagaaatc	gttgatgtta	agcgggccga	acggctcggc	gtactggggc	agacggacct					180

tgagatcaat	gagcaggacg	gtcagattac	cgctcttatc	atcccttctg	ttaaatggtt					240

cggactagga	agaaaacagg	ggaatgacat	taaggtgccc	tggtcgcaaa	ttcaaaaaat					300

cggctcggat	atgatcattt	tggatgttcc	ggaaagcagc	gtgacaaaag	aggagtaagc					360

aaggtggaaa	cccgcccgtc	ccatgggggc	gggctttttg	tttttctgga	tttcaattca					420

ctgctatttc	cttttgtca	tatgatgaaa	ttagcttatg	aattagatcc	ttgtcaaaaa					480

agaaggtgaa tgttagagcc atg tta acc gga ttg acg att gca atc atc ggc   533
                                Met Leu Thr Gly Leu Thr Ile Ala Ile Ile Gly
                                1   5   10

ggc gat gca agg cag ctc gag atc atc cgc aag ctg acg gaa cag gat   581
Gly Asp Ala Arg Gln Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp
             15   20   25

gca aag gtc ttt tta atc ggt ttt gat cag ctt gat cac ggg ttt acc   629
Ala Lys Val Phe Leu Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr
             30   35   40

gga gct aca aaa cta aag ctg aac gaa ctt gat ttt ggc aca ata gac   677
Gly Ala Thr Lys Leu Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp
             45   50   55

agc att att ctg cct gta tcg ggc aca tcg atg gaa gga acg gtt gcg   725
Ser Ile Ile Leu Pro Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala
60   65   70   75

act gtt ttt tcc aat gaa aaa gtg gtg tta aaa cag gaa cat tta gaa   773
Thr Val Phe Ser Asn Glu Lys Val Val Leu Lys Gln Glu His Leu Glu
                     80   85   90

aaa acc aag ccg cac tgc gcg att tat tca ggg att tca aac caa tat   821
Lys Thr Lys Pro His Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr
                     95   100   105

tta gac ggc atg gcc aaa ggg gcg aac cgt cgt ctt atc aag ctc ttt   869
Leu Asp Gly Met Ala Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe
             110   115   120

gaa aga gac gat att gcg att tac aac tcg ata cct aca gtc gaa ggt   917
Glu Arg Asp Asp Ile Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly
        125   130   135

gcc att atg atg gcc ata cag cat aca gac ttt acg att cac ggc tcg   965
Ala Ile Met Met Ala Ile Gln His Thr Asp Phe Thr Ile His Gly Ser
140   145   150   155

aat gta atg gtt ctc ggg ctg ggg cgg acg gga atg agc atc agc cgg   1013
Asn Val Met Val Leu Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg
                     160   165   170

acg ttc tcg gcg ctc ggc gca cgc gta aaa gtc gga gct cgc gac tcc   1061
Thr Phe Ser Ala Leu Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser
             175   180   185

gcc cac ctc gcc aga atc atg gag atg ggc ctc act cct ttc cac aca   1109
Ala His Leu Ala Arg Ile Met Glu Met Gly Leu Thr Pro Phe His Thr
             190   195   200

aac gaa ctt gca gag cat gtt gaa aat atc gac ata tgc atc aat acc   1157
Asn Glu Leu Ala Glu His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr
205   210   215

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tt cca agc ctg att ctc gat aaa cat gtc ctc tca cga atg aca ccc    1205
le Pro Ser Leu Ile Leu Asp Lys His Val Leu Ser Arg Met Thr Pro
20              225             230                 235

ga aca tta att ctc gat tta gca acc cgt ccc gga ggc aca gat ttt    1253
rg Thr Leu Ile Leu Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe
            240                 245                 250

at ttt gcc gaa aag caa ggc att aaa gcg ctg ctt gct cca gga ctt    1301
sp Phe Ala Glu Lys Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu
           255                 260                 265

cc ggg atc gtc gcg cct aaa acg gcg gga cag atc att gcc aat gtt    1349
ro Gly Ile Val Ala Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val
270                 275                 280

ttg tgc aac ctt ttg tct gaa tta aca act gac cga aag ggg ctg tca   1397
Leu Cys Asn Leu Leu Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser
285                 290                 295

taatgtcgat caaaggaaaa agaatcggat ttggcctaac gggttcacat tgtacgtatg   1457

atgccgtttt tccgcagatt gaagcgctga tcaacaaagg ggctgaagtc agaccggtcg   1517

tgacgcatac tgtcaagtcg acggatacac gctttggaga aggggaagaa tgggtcagaa   1577

gaatagaaga gctgactgga tttgaagtca ttgattccat tccgaaagct gagcctctcg   1637

ggccgaaaac accgctggac tgcatggttg ttgcgccatt gacgggaaat tcgatgagca   1697

agcttgcaaa cgcccagacg gacagtccgg ttctcatggc ggccaaagcg acgatgagaa   1757

actcccgtcc cgtcgtcctc ggcatttcaa cgaatgacgc gctcggcttg aacggcgtca   1817

acttgatgag gctgatggcg gcaaaaaatg tttactttat tccgttcggc caggatgacc   1877
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cttac
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<210> 93

<211> 299

<212> PRT

<213> Bacillus licheniformis

<400> 93

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Met Leu Thr Gly Leu Thr Ile Ala Ile Ile Gly Gly Asp Ala Arg Gln
1               5               10              15

Leu Glu Ile Ile Arg Lys Leu Thr Glu Gln Asp Ala Lys Val Phe Leu
            20              25              30

Ile Gly Phe Asp Gln Leu Asp His Gly Phe Thr Gly Ala Thr Lys Leu
            35              40              45

Lys Leu Asn Glu Leu Asp Phe Gly Thr Ile Asp Ser Ile Ile Leu Pro
        50              55              60
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Val Ser Gly Thr Ser Met Glu Gly Thr Val Ala Thr Val Phe Ser Asn
 65              70              75              80

Glu Lys Val Val Leu Lys Gln Glu His Leu Glu Lys Thr Lys Pro His
                85              90              95

Cys Ala Ile Tyr Ser Gly Ile Ser Asn Gln Tyr Leu Asp Gly Met Ala
            100             105             110

Lys Gly Ala Asn Arg Arg Leu Ile Lys Leu Phe Glu Arg Asp Asp Ile
        115             120             125

Ala Ile Tyr Asn Ser Ile Pro Thr Val Glu Gly Ala Ile Met Met Ala
    130             135             140

Ile Gln His Thr Asp Phe Thr Ile His Gly Ser Asn Val Met Val Leu
145             150             155             160

Gly Leu Gly Arg Thr Gly Met Ser Ile Ser Arg Thr Phe Ser Ala Leu
            165             170             175

Gly Ala Arg Val Lys Val Gly Ala Arg Asp Ser Ala His Leu Ala Arg
        180             185             190

Ile Met Glu Met Gly Leu Thr Pro Phe His Thr Asn Glu Leu Ala Glu
        195             200             205

His Val Glu Asn Ile Asp Ile Cys Ile Asn Thr Ile Pro Ser Leu Ile
    210             215             220

Leu Asp Lys His Val Leu Ser Arg Met Thr Pro Arg Thr Leu Ile Leu
225             230             235             240

Asp Leu Ala Thr Arg Pro Gly Gly Thr Asp Phe Asp Phe Ala Glu Lys
            245             250             255

Gln Gly Ile Lys Ala Leu Leu Ala Pro Gly Leu Pro Gly Ile Val Ala
        260             265             270

Pro Lys Thr Ala Gly Gln Ile Ile Ala Asn Val Leu Cys Asn Leu Leu
        275             280             285

Ser Glu Leu Thr Thr Asp Arg Lys Gly Leu Ser
    290             295
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<210> 94

<211> 1588

<212> DNA

<213> Bacillus licheniformis

Page 142

220>

221>   CDS

222>   (501)..(1088)

223>

400>   94

ttacctacag tcgaaggtgc cattatgatg gccatacagc atacagactt tacgattcac   60

ggctcgaatg taatggttct cgggctgggg cggacgggaa tgagcatcag ccggacgttc   120

tcggcgctcg gcgcacgcgt aaaagtcgga gctcgcgact ccgcccacct cgccagaatc   180

atggagatgg gcctcactcc tttccacaca aacgaacttg cagagcatgt tgaaaatatc   240

gacatatgca tcaataccat tccaagcctg attctcgata aacatgtcct ctcacgaatg   300

acacccagaa cattaattct cgatttagca acccgtcccg gaggcacaga ttttgatttt   360

gccgaaaagc aaggcattaa agcgctgctt gctccaggac ttcccgggat cgtcgcgcct   420

aaaacggcgg gacagatcat tgccaatgtt ttgtgcaacc ttttgtctga attaacaact   480

gaccgaaagg ggctgtcata atg tcg atc aaa gga aaa aga atc gga ttt ggc   533
                         Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly
                          1   5   10

cta acg ggt tca cat tgt acg tat gat gcc gtt ttt ccg cag att gaa   581
Leu Thr Gly Ser His Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu
            15   20   25

gcg ctg atc aac aaa ggg gct gaa gtc aga ccg gtc gtg acg cat act   629
Ala Leu Ile Asn Lys Gly Ala Glu Val Arg Pro Val Val Thr His Thr
            30   35   40

gtc aag tcg acg gat aca cgc ttt gga gaa ggg gaa gaa tgg gtc aga   677
Val Lys Ser Thr Asp Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg
        45   50   55

aga ata gaa gag ctg act gga ttt gaa gtc att gat tcc att ccg aaa   725
Arg Ile Glu Glu Leu Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys
60   65   70   75

gct gag cct ctc ggg ccg aaa aca ccg ctg gac tgc atg gtt gtt gcg   773
Ala Glu Pro Leu Gly Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala
                80   85   90

cca ttg acg gga aat tcg atg agc aag ctt gca aac gcc cag acg gac   821
Pro Leu Thr Gly Asn Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp
                95   100   105

agt ccg gtt ctc atg gcg gcc aaa gcg acg atg aga aac tcc cgt ccc   869
Ser Pro Val Leu Met Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro
            110   115   120

gtc gtc ctc ggc att tca acg aat gac gcg ctc ggc ttg aac ggc gtc   917
Val Val Leu Gly Ile Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val
            125   130   135

aac ttg atg agg ctg atg gcg gca aaa aat gtt tac ttt att ccg ttc   965
Asn Leu Met Arg Leu Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe
140   145   150   155

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ggc cag gat gac cct tac aaa aag ccg aat tcg ctc gtc gcc aaa atg    1013
Gly Gln Asp Asp Pro Tyr Lys Lys Pro Asn Ser Leu Val Ala Lys Met
                160             165                 170

gat ctt tta gtg ccg gcg gtc gaa gaa gcg ctc tcc cat aaa caa ata    1061
Asp Leu Leu Val Pro Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile
                175             180                 185

cag cct atc ctg gtc cat aat gat caa taaatctttt gaaaataaag          1108
Gln Pro Ile Leu Val His Asn Asp Gln
                190             195

atgtaacaaa aaatatcaat caccacggca cacatctatg ttaaaataaa atgtaaaatg  1168

catagtcaac caatcgttta cgacgattaa ggtggaagga gttttacaat tgggcagagg  1228

attacatgta gcagtagttg gtgcgacagg cgctgtagga cagcaaatgt taaaaacact  1288

agaagacagg aattttgaac tggataaact gactttatta tcctcaaaac gttcagcagg  1348

tacgaaactg actttcaaag gcgaagagta cacagtagaa gaagctcgtc ctgagagctt  1408

tgaaggcgtc aacatcgcgc ttttcagcgc cggggggaagc gtttcgcagg cgcttgctca  1468

cgaggctgtc aaacgcgggg cgatcgtcat tgataatacg agcgcgttcc ggatggacca  1528

aaacactccg ctcgtcgtac ctgaggtcaa tgaggaagat ttgcacaagc acaacgggat  1588
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<210> 95

<211> 196

<212> PRT

<213> Bacillus licheniformis

<400> 95

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Met Ser Ile Lys Gly Lys Arg Ile Gly Phe Gly Leu Thr Gly Ser His
1               5               10                  15


Cys Thr Tyr Asp Ala Val Phe Pro Gln Ile Glu Ala Leu Ile Asn Lys
                20              25                  30


Gly Ala Glu Val Arg Pro Val Val Thr His Thr Val Lys Ser Thr Asp
            35                  40                  45


Thr Arg Phe Gly Glu Gly Glu Glu Trp Val Arg Arg Ile Glu Glu Leu
        50                  55                  60


Thr Gly Phe Glu Val Ile Asp Ser Ile Pro Lys Ala Glu Pro Leu Gly
65                  70                  75                  80


Pro Lys Thr Pro Leu Asp Cys Met Val Val Ala Pro Leu Thr Gly Asn
                85                  90                  95


Ser Met Ser Lys Leu Ala Asn Ala Gln Thr Asp Ser Pro Val Leu Met
                100                 105                 110
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Page 144

Ala Ala Lys Ala Thr Met Arg Asn Ser Arg Pro Val Val Leu Gly Ile
        115   120   125

Ser Thr Asn Asp Ala Leu Gly Leu Asn Gly Val Asn Leu Met Arg Leu
        130   135   140

Met Ala Ala Lys Asn Val Tyr Phe Ile Pro Phe Gly Gln Asp Asp Pro
145   150   155   160

Tyr Lys Lys Pro Asn Ser Leu Val Ala Lys Met Asp Leu Leu Val Pro
                165   170   175

Ala Val Glu Glu Ala Leu Ser His Lys Gln Ile Gln Pro Ile Leu Val
            180   185   190

His Asn Asp Gln
        195

<210>   96

<211>   2167

<212>   DNA

<213>   Bacillus licheniformis

<220>

<221>   CDS

<222>   (501)..(1871)

<223>

<400>   96
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aggaatttct gaagctgcag agaaaaatgg cattccgtgt acattcaaca gggcggggtc   120

tatgatcggc tttttcttca caaatggacc ggtcatcaat tatgatacag cgaaacagtc   180

tgacctcgga ctgtttgccg aatattataa aggaatggcc gatgaaggcg tgtttctgcc   240

gccttcacag tttgaagggc tgttcttgtc aaccgctcat acggatgacg acattgagca   300

tacgattaaa gctgctgaac gcgtattcga aagaatcagc cgctccagat aaagaaaagg   360

gctgccggac attgccggcg ctctttttt gcatggtgcc gaaaacggct gctgattttt   420

ctgttcatat tctgcctgct tttcacatac atctttactg acatctaatt ttaaaaatta   480

ggtgaaggga ggatatcagt ttg ccg caa aac aat cgt ttg caa ttt tct gta   533
                      Leu Pro Gln Asn Asn Arg Leu Gln Phe Ser Val
                       1   5   10

gaa gag tca atc tgt ttt caa aaa gga cag gaa gta tcc gaa tta tta   581

Glu Glu Ser Ile Cys Phe Gln Lys Gly Gln Glu Val Ser Glu Leu Leu
          15   20   25

tcg att tca ttg gat cct gac att acc gtt cag gaa gta aat gat tat   629
Ser Ile Ser Leu Asp Pro Asp Ile Thr Val Gln Glu Val Asn Asp Tyr
        30   35   40

gta tcc ata cga ggg tca tta gag ctg aca ggc gaa tac aac ata gat   677
Val Ser Ile Arg Gly Ser Leu Glu Leu Thr Gly Glu Tyr Asn Ile Asp
        45   50   55

caa acc cgg gag tat gca gag ctg cct gcg aca agc cga ttt gta gaa   725
Gln Thr Arg Glu Tyr Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu
60   65   70   75

gat gta aag ctg aaa ggg gac ggc agc gca gag ctg acg cat tgt ttc   773
Asp Val Lys Leu Lys Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe
            80   85   90

cca gtg gat atc acc atc ccg aaa gac aaa gtc aat cat tta aac gac   821
Pro Val Asp Ile Thr Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp
        95   100   105

gta ttt gtt ttt att gac gct ttc gat tat cag ctg aca gat gcg agg   869
Val Phe Val Phe Ile Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg
       110   115   120

atg ctg acg att cag gct gat ttg gcg att gaa ggc ctc ttg aat gtg   917
Met Leu Thr Ile Gln Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val
       125   130   135

agc ggt gaa gcg ggt gaa gaa gaa ccg cgc act atg cct gcg gcc gtc   965
Ser Gly Glu Ala Gly Glu Glu Glu Pro Arg Thr Met Pro Ala Ala Val
140   145   150   155

cat ccg gaa gag gag ctc gaa cct gcc tac aga tca cct tca aac gac   1013
His Pro Glu Glu Glu Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp
            160   165   170

gaa gat cag ggt gaa gag aaa gaa tat ttg atc cag ctt gac aga cct   1061
Glu Asp Gln Gly Glu Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro
            175   180   185

tac gaa gag cag gac gaa gaa cag gcg gaa gaa cat gat acc ggt gag   1109
Tyr Glu Glu Gln Asp Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu
       190   195   200

gaa acg gtt ccg att tac cag tcg ttt ctc gga aac gac aca gag gaa   1157
Glu Thr Val Pro Ile Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu
       205   210   215

gct aaa ccg ttt ttt aca gcg tct ttg tcg gcg gca gag cgt acg aag   1205
Ala Lys Pro Phe Phe Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys
220   225   230   235

cgc gaa ata gaa aat caa aaa gaa gcc tct ctt gaa cag ccg gaa gaa   1253
Arg Glu Ile Glu Asn Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu
            240   245   250

gaa tat aag ctg aaa aga gag aaa gtg gaa gag gaa ccg gaa gaa tat   1301
Glu Tyr Lys Leu Lys Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr
       255   260   265

gag ctg aaa aga gag aaa gtg gaa gag gaa ccg gaa gaa tat gag ctg   1349
Glu Leu Lys Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu
       270   275   280

aaa aga gaa gaa gcg gaa gaa gag ccg gag ctg tcg cac agc tct tat   1397

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Lys Arg Glu Glu Ala Glu Glu Glu Pro Glu Leu Ser His Ser Ser Tyr
285             290                 295

caa cct cac gag gaa ctg aaa gag aac ccg ttc tac agt gtt cct cct    1445
Gln Pro His Glu Glu Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro
300                 305                 310                 315

ctt ctg aag gaa gac cag aat gac agg gag cct gag gct ttt gag gtt    1493
Leu Leu Lys Glu Asp Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val
                320                 325                 330

gag gtg aca cag gaa gca gaa gcg att gat gaa gaa gag gaa gcc ggg    1541
Glu Val Thr Gln Glu Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly
                335                 340                 345

cat acg att gaa atc ccg gaa tat tcg ttt cat gag cag acg gag ccc    1589
His Thr Ile Glu Ile Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro
            350                 355                 360

gaa gaa gaa aga gat gaa atg cag gca gcg gat gaa cag gaa gtg tca    1637
Glu Glu Glu Arg Asp Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser
365                 370                 375

gca aag gaa aac gac aac gca ctc tat ttg aca aag ctg ttt aca aag    1685
Ala Lys Glu Asn Asp Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys
380                 385                 390                 395

cag gga gag gag gag ttt act cga atg agg atg tgc atc gtt cag caa    1733
Gln Gly Glu Glu Glu Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln
                400                 405                 410

aat gat acg att gat ctt ctg tgc gag cgc tat gat att aac gtc cag    1781
Asn Asp Thr Ile Asp Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln
                415                 420                 425

cag ctc atc cgg atg aat tcc ctt tcc ctt gac gag gaa tta aaa gag    1829
Gln Leu Ile Arg Met Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu
            430                 435                 440

gga cag atc ctt tat ata ccg gat tat caa aac agc cat gcc            1871
Gly Gln Ile Leu Tyr Ile Pro Asp Tyr Gln Asn Ser His Ala
445                 450                 455

taatgcattg ataaaaatgt ggtgaagccg atggaaggca tccagtctgt tttaaatgag    1931

tacggtctta cgcctgaata tatggagtcc gtcagttcaa aggtgtggaa agtgtatacg    1991

gatcacggtg tatttgctct gaaaaaattg gcggcttcaa gaaacacccg cttcacggaa    2051

cagatgatca tgctggagga aaaaggctac aggcagttcg ttcctgtcta tcgaaaccgc    2111

acaggcgaat ttttaacgca agccggagaa gatgtctgct atctcatgcc ctggct        2167
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<210> 97

<211> 457

<212> PRT

<213> Bacillus licheniformis

<400> 97

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Phe Gln Lys Gly Gln Glu Val Ser Glu Leu Leu Ser Ile Ser Leu Asp
                20   25   30

Pro Asp Ile Thr Val Gln Glu Val Asn Asp Tyr Val Ser Ile Arg Gly
        35   40   45

Ser Leu Glu Leu Thr Gly Glu Tyr Asn Ile Asp Gln Thr Arg Glu Tyr
    50   55   60

Ala Glu Leu Pro Ala Thr Ser Arg Phe Val Glu Asp Val Lys Leu Lys
65   70   75   80

Gly Asp Gly Ser Ala Glu Leu Thr His Cys Phe Pro Val Asp Ile Thr
            85   90   95

Ile Pro Lys Asp Lys Val Asn His Leu Asn Asp Val Phe Val Phe Ile
        100   105   110

Asp Ala Phe Asp Tyr Gln Leu Thr Asp Ala Arg Met Leu Thr Ile Gln
        115   120   125

Ala Asp Leu Ala Ile Glu Gly Leu Leu Asn Val Ser Gly Glu Ala Gly
    130   135   140

Glu Glu Glu Pro Arg Thr Met Pro Ala Ala Val His Pro Glu Glu Glu
145   150   155   160

Leu Glu Pro Ala Tyr Arg Ser Pro Ser Asn Asp Glu Asp Gln Gly Glu
            165   170   175

Glu Lys Glu Tyr Leu Ile Gln Leu Asp Arg Pro Tyr Glu Glu Gln Asp
            180   185   190

Glu Glu Gln Ala Glu Glu His Asp Thr Gly Glu Glu Thr Val Pro Ile
        195   200   205

Tyr Gln Ser Phe Leu Gly Asn Asp Thr Glu Glu Ala Lys Pro Phe Phe
    210   215   220

Thr Ala Ser Leu Ser Ala Ala Glu Arg Thr Lys Arg Glu Ile Glu Asn
    225   230   235   240

Gln Lys Glu Ala Ser Leu Glu Gln Pro Glu Glu Glu Tyr Lys Leu Lys
            245   250   255

Arg Glu Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu
            260   265   270

Lys Val Glu Glu Glu Pro Glu Glu Tyr Glu Leu Lys Arg Glu Glu Ala
    275   280   285

Page 148

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Glu Glu Glu Pro Glu Leu Ser His Ser Ser Tyr Gln Pro His Glu Glu
    290                 295                 300

Leu Lys Glu Asn Pro Phe Tyr Ser Val Pro Pro Leu Leu Lys Glu Asp
305                 310                 315                 320

Gln Asn Asp Arg Glu Pro Glu Ala Phe Glu Val Glu Val Thr Gln Glu
                325                 330                 335

Ala Glu Ala Ile Asp Glu Glu Glu Glu Ala Gly His Thr Ile Glu Ile
                340                 345                 350

Pro Glu Tyr Ser Phe His Glu Gln Thr Glu Pro Glu Glu Glu Arg Asp
            355                 360                 365

Glu Met Gln Ala Ala Asp Glu Gln Glu Val Ser Ala Lys Glu Asn Asp
    370                 375                 380

Asn Ala Leu Tyr Leu Thr Lys Leu Phe Thr Lys Gln Gly Glu Glu Glu
385                 390                 395                 400

Phe Thr Arg Met Arg Met Cys Ile Val Gln Gln Asn Asp Thr Ile Asp
                405                 410                 415

Leu Leu Cys Glu Arg Tyr Asp Ile Asn Val Gln Gln Leu Ile Arg Met
            420                 425                 430

Asn Ser Leu Ser Leu Asp Glu Glu Leu Lys Glu Gly Gln Ile Leu Tyr
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Ile Pro Asp Tyr Gln Asn Ser His Ala
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<210> 98

<211> 1955

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1463)

<223>

<400> 98
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aaaaaggcga atttcatttc cttcaaatca aaaagacttt ggtgaagatc ccgctgtgaa   180

acaggggaga gccgagcagc gcctgcagca catcttcaga cagattggct ccattccccg   240

aaggacctca tcaatcacca ctttctcccg atttgccatg tcaacctgtt aagcatttac   300

caaacaggat gaaaaaattg gtttgtccgc acagcttacc tgaatacaat aaaaaataaa   360

gtatttctcg ggaaagcgca ggtttcaaca agacctgccc cgttcttgtc aaaaagcatt   420

ggattgtgca gtcatgtggg cgtctgtcac ggcataagcg cgccatgaat aggatataaa   480

gagagaatgg tgaggtgagt gtg ttg gaa agg gct gtt act tat aaa aac aac   533
                                    Val Leu Glu Arg Ala Val Thr Tyr Lys Asn Asn
                                    1   5   10

gga caa atc aat atc ata ttg aac ggt caa aag cag gtt ttg gcc aat   581
Gly Gln Ile Asn Ile Ile Leu Asn Gly Gln Lys Gln Val Leu Ala Asn
            15   20   25

tca gag gct gaa gcc gaa tat cag gcc gca ctg caa aaa aat gaa gcc   629
Ser Glu Ala Glu Ala Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala
            30   35   40

aaa cac agc att ctg aaa gaa att gaa agg gaa atg aac acg ctg gtc   677
Lys His Ser Ile Leu Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val
            45   50   55

gga atg gag gaa atg aag cgc aat atc aag gaa atc tac gcc tgg att   725
Gly Met Glu Glu Met Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile
60   65   70   75

ttc gtt aat aaa aag cgc gaa gaa caa ggc ctt aag gcc gga aaa cag   773
Phe Val Asn Lys Lys Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln
                80   85   90

gcg ctt cac atg atg ttc aaa gga aat ccg gga acc gga aaa acg acc   821
Ala Leu His Met Met Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr
            95   100   105

gtc gcc agg ctg atc ggc agg ctt ttt tac gaa atg aat gtt ctc tca   869
Val Ala Arg Leu Ile Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser
           110   115   120

aaa ggc cat ctg atc gag gcg gag cgc gcc gat ctc gtc ggt gag tac   917
Lys Gly His Leu Ile Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr
           125   130   135

atc ggc cat acg gcg caa aaa acg agg gat tta atc aaa aaa gcg atg   965
Ile Gly His Thr Ala Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met
140   145   150   155

ggc gga atc ctg ttc atc gat gaa gcc tat tcc ctt gcc aga ggc gga   1013
Gly Gly Ile Leu Phe Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly
                160   165   170

gag aaa gac ttc ggc aag gag gca atc gat aca ttg gtc aaa cat atg   1061
Glu Lys Asp Phe Gly Lys Glu Ala Ile Asp Thr Leu Val Lys His Met
                175   180   185

gag gat aag cgc aac gaa ttc att tta atc ctc gcc gga tat tcg cgg   1109
Glu Asp Lys Arg Asn Glu Phe Ile Leu Ile Leu Ala Gly Tyr Ser Arg
           190   195   200

gaa atg gat cat ttt ctt tca tta aac ccg ggc ctt cag tca agg ttt   1157

| Glu | Met | Asp | His | Phe | Leu | Ser | Leu | Asn | Pro | Gly | Leu | Gln | Ser | Arg | Phe | |
| | 205 | | | | 210 | | | | | 215 | | | | | | |

ccg	atc	agc	atc	gat	ttt	ccc	gat	tac	tca	gtc	agc	cag	ctg	atg	gac	1205
Pro	Ile	Ser	Ile	Asp	Phe	Pro	Asp	Tyr	Ser	Val	Ser	Gln	Leu	Met	Asp	
220					225					230					235	

att	gca	aaa	cgg	atg	atg	gcg	gaa	agg	gaa	tat	cag	ttc	agc	cct	gag	1253
Ile	Ala	Lys	Arg	Met	Met	Ala	Glu	Arg	Glu	Tyr	Gln	Phe	Ser	Pro	Glu	
				240					245					250		

gct	gaa	tgg	aag	ctg	aaa	gac	cat	ctg	atg	gcc	gtc	aaa	agt	acg	gtc	1301
Ala	Glu	Trp	Lys	Leu	Lys	Asp	His	Leu	Met	Ala	Val	Lys	Ser	Thr	Val	
			255					260					265			

agc	ccc	gcg	aag	ttc	agc	aat	ggc	cgt	ttc	gtc	cgc	aac	ctg	atc	gaa	1349
Ser	Pro	Ala	Lys	Phe	Ser	Asn	Gly	Arg	Phe	Val	Arg	Asn	Leu	Ile	Glu	
		270					275					280				

aaa	tcc	atc	cgg	tcg	cag	gcg	atg	aga	ctg	ctg	atg	gga	gac	tgc	tac	1397
Lys	Ser	Ile	Arg	Ser	Gln	Ala	Met	Arg	Leu	Leu	Met	Gly	Asp	Cys	Tyr	
	285				290					295						

tta	aag	aat	gac	ttg	ata	acc	atc	aaa	agc	cag	gat	ctc	gac	ttg	aag	1445
Leu	Lys	Asn	Asp	Leu	Ile	Thr	Ile	Lys	Ser	Gln	Asp	Leu	Asp	Leu	Lys	
300					305					310					315	

gaa	gac	gcg	ccg	cac	gta	taatggcgcg	ttcttttttt	attttcgagg								1493
Glu	Asp	Ala	Pro	His	Val											
			320													

atttctggca	accgctccct	tcgtttgtta	tgatagtact	gcttattgac	taacgttaag	1553
aaaggaacat	gatcacttga	acgaacagga	agtcatgaaa	gagaaagcca	tattagtcgg	1613
atgccagctt	ccgcacgtgt	ctgatgagcg	tttttcatac	tcgatggaag	agctcgccgc	1673
gctgacgaaa	acggccgacg	gaacggttgt	ttccacggtc	acgcagaagc	ggaaccgtgt	1733
ggatgctgct	acatatatcg	gaaaaggaaa	agtagatgaa	ttggcggtgc	tctgtgaaga	1793
gctgtcgccc	gatgtttttaa	tttttaatga	tgaattgtcg	ccgagtcagc	tgaaagcgct	1853
tgtcacaacg	cttgacgtga	aaatcatcga	ccggacgcag	ttgatccttg	atattttcgc	1913
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<210> 99

<211> 321

<212> PRT

<213> Bacillus licheniformis

<400> 99

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| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| Ile | Leu | Asn | Gly | Gln | Lys | Gln | Val | Leu | Ala | Asn | Ser | Glu | Ala | Glu | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |

Page 151

Glu Tyr Gln Ala Ala Leu Gln Lys Asn Glu Ala Lys His Ser Ile Leu
        35   40   45

Lys Glu Ile Glu Arg Glu Met Asn Thr Leu Val Gly Met Glu Glu Met
    50   55   60

Lys Arg Asn Ile Lys Glu Ile Tyr Ala Trp Ile Phe Val Asn Lys Lys
65   70   75   80

Arg Glu Glu Gln Gly Leu Lys Ala Gly Lys Gln Ala Leu His Met Met
                85   90   95

Phe Lys Gly Asn Pro Gly Thr Gly Lys Thr Thr Val Ala Arg Leu Ile
            100   105   110

Gly Arg Leu Phe Tyr Glu Met Asn Val Leu Ser Lys Gly His Leu Ile
        115   120   125

Glu Ala Glu Arg Ala Asp Leu Val Gly Glu Tyr Ile Gly His Thr Ala
    130   135   140

Gln Lys Thr Arg Asp Leu Ile Lys Lys Ala Met Gly Gly Ile Leu Phe
145   150   155   160

Ile Asp Glu Ala Tyr Ser Leu Ala Arg Gly Gly Glu Lys Asp Phe Gly
                165   170   175

Lys Glu Ala Ile Asp Thr Leu Val Lys His Met Glu Asp Lys Arg Asn
            180   185   190

Glu Phe Ile Leu Ile Leu Ala Gly Tyr Ser Arg Glu Met Asp His Phe
        195   200   205

Leu Ser Leu Asn Pro Gly Leu Gln Ser Arg Phe Pro Ile Ser Ile Asp
    210   215   220

Phe Pro Asp Tyr Ser Val Ser Gln Leu Met Asp Ile Ala Lys Arg Met
225   230   235   240

Met Ala Glu Arg Glu Tyr Gln Phe Ser Pro Glu Ala Glu Trp Lys Leu
                245   250   255

Lys Asp His Leu Met Ala Val Lys Ser Thr Val Ser Pro Ala Lys Phe
        260   265   270

Ser Asn Gly Arg Phe Val Arg Asn Leu Ile Glu Lys Ser Ile Arg Ser
        275   280   285

Gln Ala Met Arg Leu Leu Met Gly Asp Cys Tyr Leu Lys Asn Asp Leu
290   295   300

Page 152

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Ile Thr Ile Lys Ser Gln Asp Leu Asp Leu Lys Glu Asp Ala Pro His
305              310              315              320

Val
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<210> 100

<211> 2082

<212> DNA

<213> Bacillus licheniformis

<220>

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<222> (501)..(1607)

<223>

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aggcgggaat acaaggccgc tatctactgg tatgagctgg ccacaacatt ggtgcctgat   180

tcaaataaat ggagcttcac ctatccggca tactatactt ggtaccctca tttgcaaatg   240

tgtgtgtgct attacaattt aggagacttt gaaaagtcgt atcatcataa tgaagaggcg   300

aggaaatacc gtcccgaaga caaatccgtc cttcataaca aacagctgct ggaagggaaa   360

ttaggcatta acaattagca ttgtaaagac ttactgaaca agtaggtctt ttttttatga   420

ataaaatcaa gccgtgccaa tttagcggca ggcatcataa cttattttgg aactttttga   480

atttagagga ggaacaaagg atg atc ccg tta gtc aat tta aaa cgt caa ttt   533
                       Met Ile Pro Leu Val Asn Leu Lys Arg Gln Phe
                        1               5                  10

caa aca gta aaa cag gat att tta aaa gag ttt gaa cat gtg ctg gac     581
Gln Thr Val Lys Gln Asp Ile Leu Lys Glu Phe Glu His Val Leu Asp
            15              20                  25

agc ggc caa tat ata ttg ggg cca aag gtt gaa gaa tta gag aaa aga     629
Ser Gly Gln Tyr Ile Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg
            30              35              40

ata gct gaa aag ctt ggt gta aaa gaa gcg gtc gcg gtc gcc aac gga     677
Ile Ala Glu Lys Leu Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly
        45              50              55

acg gat gca ttg gtg ctg acg ctt gaa gct ttc ggc atc ggc aaa ggg     725
Thr Asp Ala Leu Val Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly
60              65              70              75

gat gaa gtg att acg acc ccg ttc act ttt ttc gcc acc gcc gaa gcc     773
Asp Glu Val Ile Thr Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala
                80              85              90
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gtc tca agg gtg ggg gct gaa cct gtg ttt gct gat gtc gat cct gaa      821
Val Ser Arg Val Gly Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu
            95              100                 105

aca tac aat ctt gat ccg aaa aaa ata gaa gaa aag atc acc cct gct      869
Thr Tyr Asn Leu Asp Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala
            110             115                 120

act aaa gcg atc att ccc gtc cat atc ttc gga cag ccg gct gat atg      917
Thr Lys Ala Ile Ile Pro Val His Ile Phe Gly Gln Pro Ala Asp Met
    125                 130                 135

gac gag atc atg gag ctt gcc aaa aaa cac gga ctg ctt gtg att gag      965
Asp Glu Ile Met Glu Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu
140                 145                 150                 155

gat gcc tgc caa gcg ttc ggc gca tcg tat aaa gag cgg cct gtc ggc     1013
Asp Ala Cys Gln Ala Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly
                160                 165                 170

agc atc ggg gat gcc gcc tgt ttt tca ttt ttc cct aca aaa aac ttg     1061
Ser Ile Gly Asp Ala Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu
                175                 180                 185

gga aca ttg gga gac ggg gga atg gtg acg att tca gac ccg gat gca     1109
Gly Thr Leu Gly Asp Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala
            190                 195                 200

gcc cgg caa tta aga aca ctc aga acc cat ggc act agc aaa aaa tac     1157
Ala Arg Gln Leu Arg Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr
    205                 210                 215

ttc cat gac aaa atc ggt ttc aac agc cgt ctt gat gaa tta cac gcc     1205
Phe His Asp Lys Ile Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala
220                 225                 230                 235

gca gct tta ctc att ctt ctt gag aaa atc gac ggc tgg aat gaa caa     1253
Ala Ala Leu Leu Ile Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln
                240                 245                 250

aga aga aga gtg gcc agc cgc tac aga gaa ggt ttg aaa acg gcg gag     1301
Arg Arg Arg Val Ala Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu
                255                 260                 265

cac ctc aca ctg ccg gca gag aaa gag gac cgc aca cat atc tat cat     1349
His Leu Thr Leu Pro Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His
            270                 275                 280

ctc tat tgt atc ggc gcg aaa aac cgc gac tac atc ata caa tcg ctg     1397
Leu Tyr Cys Ile Gly Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu
285                 290                 295

aaa gag cag gac att cat tca ggt gtg tat tat cct tgc tgc ctt cat     1445
Lys Glu Gln Asp Ile His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His
300                 305                 310                 315

ctg caa tcg gtc tat tct tca ctg cag tac aaa aaa ggc gat ttt cct     1493
Leu Gln Ser Val Tyr Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro
                320                 325                 330

ata gcc gag tcc ttg tcc gaa acc ctt ttc gcc att ccg atg gat cct     1541
Ile Ala Glu Ser Leu Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro
                335                 340                 345

ttt cta gcc gcc gag gaa caa gat cag att att tct gcg ctg ctg aaa     1589
Phe Leu Ala Ala Glu Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys
        350                 355                 360
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Page 154

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aaa gga gga ggg gaa aag tgacggttca ttttggttta atcggctgcg      1637
Lys Gly Gly Gly Glu Lys
         365

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ccgtcagtga tttgcaggaa gaaagaatga aggaagcgga agaatactat gcttccctcg    1757

ccggtgagga aagccgaatg acccgctatc cgcagtatca agcgctgctt tcagatccta    1817

aaattgaagc ggtcattatt gcggcggttt cgggactgca cgccgaaatg gccaaacatg    1877

cgctgctggc aggcaagcac gtcatcgtcg aaaaaccgat gaccttgtca ttacgggatg    1937

ccgatgagct tatagaactg gcggagcaga acgggctgaa gctcatggtc tgccaccaga    1997

tgcgccaccg gccgatcatg aaaaaactga aggaaacgat tgaggaagga aagctgggaa    2057

                                                               2082
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<210> 101

<211> 369

<212> PRT

<213> Bacillus licheniformis

<400> 101

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Leu Gly Pro Lys Val Glu Glu Leu Glu Lys Arg Ile Ala Glu Lys Leu
        35                  40                  45

Gly Val Lys Glu Ala Val Ala Val Ala Asn Gly Thr Asp Ala Leu Val
    50                  55                  60

Leu Thr Leu Glu Ala Phe Gly Ile Gly Lys Gly Asp Glu Val Ile Thr
65                  70                  75                  80

Thr Pro Phe Thr Phe Phe Ala Thr Ala Glu Ala Val Ser Arg Val Gly
                85                  90                  95

Ala Glu Pro Val Phe Ala Asp Val Asp Pro Glu Thr Tyr Asn Leu Asp
            100                 105                 110

Pro Lys Lys Ile Glu Glu Lys Ile Thr Pro Ala Thr Lys Ala Ile Ile
        115                 120                 125

Pro Val His Ile Phe Gly Gln Pro Ala Asp Met Asp Glu Ile Met Glu
    130                 135                 140
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Leu Ala Lys Lys His Gly Leu Leu Val Ile Glu Asp Ala Cys Gln Ala
145   150   155   160

Phe Gly Ala Ser Tyr Lys Glu Arg Pro Val Gly Ser Ile Gly Asp Ala
            165   170   175

Ala Cys Phe Ser Phe Phe Pro Thr Lys Asn Leu Gly Thr Leu Gly Asp
            180   185   190

Gly Gly Met Val Thr Ile Ser Asp Pro Asp Ala Ala Arg Gln Leu Arg
            195   200   205

Thr Leu Arg Thr His Gly Thr Ser Lys Lys Tyr Phe His Asp Lys Ile
210   215   220

Gly Phe Asn Ser Arg Leu Asp Glu Leu His Ala Ala Ala Leu Leu Ile
225   230   235   240

Leu Leu Glu Lys Ile Asp Gly Trp Asn Glu Gln Arg Arg Arg Val Ala
            245   250   255

Ser Arg Tyr Arg Glu Gly Leu Lys Thr Ala Glu His Leu Thr Leu Pro
            260   265   270

Ala Glu Lys Glu Asp Arg Thr His Ile Tyr His Leu Tyr Cys Ile Gly
            275   280   285

Ala Lys Asn Arg Asp Tyr Ile Ile Gln Ser Leu Lys Glu Gln Asp Ile
            290   295   300

His Ser Gly Val Tyr Tyr Pro Cys Cys Leu His Leu Gln Ser Val Tyr
305   310   315   320

Ser Ser Leu Gln Tyr Lys Lys Gly Asp Phe Pro Ile Ala Glu Ser Leu
            325   330   335

Ser Glu Thr Leu Phe Ala Ile Pro Met Asp Pro Phe Leu Ala Ala Glu
            340   345   350

Glu Gln Asp Gln Ile Ile Ser Ala Leu Leu Lys Lys Gly Gly Gly Glu
            355   360   365

Lys

<210> 102

<211> 1975

<212> DNA

Page 156

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1472)

<223>

<400> 102

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ccaaaaggct gatttgatca ttgatcagct tcatatcggc agctacggat tatttgccgt   180

cgaatcgatg gcaatgggga aacccgttat ctgctggatc agtgatttta tgaaggatca   240

ctatccttcc gaactgcctc ttataagagc aaatcccgcc aacattacag aggtgattga   300

aaatgtgctt aaaaaccggg atatgctgcc ggaaatcggc agaaaggaa gaaagtatgc    360

agaagttcat catgatatgg tgaaaaacag caaaaaaaca ttggctgttt atcagtcgct   420

actttcggaa tgaagttgaa caactttccc gtcgcgggat ttgtatgtaa aaaaaaacga   480

aacaagcagg tgaacaattg atg agc gat atg aca gag tta tcc ggc cag cat   533
                       Met Ser Asp Met Thr Glu Leu Ser Gly Gln His
                        1               5                   10

att ttc ata act ggc gga gca ggc ttt atc gga tcc tct tta ata gga   581
Ile Phe Ile Thr Gly Gly Ala Gly Phe Ile Gly Ser Ser Leu Ile Gly
             15              20                  25

aag ctg ata gag cgc aac agc gtc acc gta tat gac aat ttt tca aga   629
Lys Leu Ile Glu Arg Asn Ser Val Thr Val Tyr Asp Asn Phe Ser Arg
         30                  35                  40

gac tcc ctc cgg tat aag cct tac cgg gac cat cct cac ttg aaa gtg   677
Asp Ser Leu Arg Tyr Lys Pro Tyr Arg Asp His Pro His Leu Lys Val
     45                  50                  55

ctg cag gga gac att ttg gat ttg aac gcg ctt aaa aag gcg atc cag   725
Leu Gln Gly Asp Ile Leu Asp Leu Asn Ala Leu Lys Lys Ala Ile Gln
 60                  65                  70                  75

ggg gcc agc cac att gtc cac gcc gcc ggc atc gct ggg att gac acg   773
Gly Ala Ser His Ile Val His Ala Ala Gly Ile Ala Gly Ile Asp Thr
                 80                  85                  90

gtc att caa aac ccg gtt aaa acg atg cag gtc aac atg atc ggt tca   821
Val Ile Gln Asn Pro Val Lys Thr Met Gln Val Asn Met Ile Gly Ser
                 95                 100                 105

gcc aat ctg ctt gaa gcg gct gcc ggt tta acc gaa tgc aaa agg gtt   869
Ala Asn Leu Leu Glu Ala Ala Ala Gly Leu Thr Glu Cys Lys Arg Val
             110                 115                 120

gtc tgt ttc agt aca agc gaa gtg ttc ggc caa atc gct ttc aga gcg   917
Val Cys Phe Ser Thr Ser Glu Val Phe Gly Gln Ile Ala Phe Arg Ala
     125                 130                 135

cgc gag acc agt cat act gtt tta gga gcg gtg gga gaa gcc cgc tgg   965
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```
Arg Glu Thr Ser His Thr Val Leu Gly Ala Val Gly Glu Ala Arg Trp
140             145             150             155

aca tat gct gtc agc aaa ctc gcc gag gag cat atg gca tat gcc tat    1013
Thr Tyr Ala Val Ser Lys Leu Ala Glu Glu His Met Ala Tyr Ala Tyr
            160             165             170

ttt aaa gaa ctt ggg ctt ccg acc gtc acc gtc cgc cct ttt aat gtt    1061
Phe Lys Glu Leu Gly Leu Pro Thr Val Thr Val Arg Pro Phe Asn Val
            175             180             185

tat gga ccg gaa caa gtc ggc gaa ggc gcc atc aaa acg atg gtt cac    1109
Tyr Gly Pro Glu Gln Val Gly Glu Gly Ala Ile Lys Thr Met Val His
            190             195             200

aga gct ctg tta gat gag ccg atc tat att cac ggc gat gga acg caa    1157
Arg Ala Leu Leu Asp Glu Pro Ile Tyr Ile His Gly Asp Gly Thr Gln
            205             210             215

atc cgg gcc tgg tgt tac gta gat gac atg atc gac gga att ttg cgt    1205
Ile Arg Ala Trp Cys Tyr Val Asp Asp Met Ile Asp Gly Ile Leu Arg
220             225             230             235

tgt ttg acg atg aag gaa gcc atc gga gag tct ttc aac atc ggc aat    1253
Cys Leu Thr Met Lys Glu Ala Ile Gly Glu Ser Phe Asn Ile Gly Asn
            240             245             250

gaa cgc act gtg atc acc gta tac gga ttg gca agc acg att atc aga    1301
Glu Arg Thr Val Ile Thr Val Tyr Gly Leu Ala Ser Thr Ile Ile Arg
            255             260             265

gtt ctc gga tca aaa tca caa atc ttc ttt ggg gag aaa aaa gaa gcc    1349
Val Leu Gly Ser Lys Ser Gln Ile Phe Phe Gly Glu Lys Lys Glu Ala
            270             275             280

gat att gaa ctg cgc atc cct cag gtc aat aaa gca aaa gag atg ctc    1397
Asp Ile Glu Leu Arg Ile Pro Gln Val Asn Lys Ala Lys Glu Met Leu
285             290             295

ggt ttc agc gct aaa gtt gat ctg gaa gaa ggc atc aga aga aca gct    1445
Gly Phe Ser Ala Lys Val Asp Leu Glu Glu Gly Ile Arg Arg Thr Ala
300             305             310             315

gaa agc att aaa aaa aat ttg gat caa taagaaagga ggcgctattg          1492
Glu Ser Ile Lys Lys Asn Leu Asp Gln
            320

ttgaaacaat ggaaaagcga aggaaaaggt gaattcactc tttcccagct tggggggctgt    1552

ggcgaaaatg tcgttatcga agacggggtc cgcatttttc atccggaaaa catctatatc      1612

ggagataacg tttatatcgg ccatgacacg attttaaaag ctattataa gcatgacctg       1672

atcatcggtt caaacagctg gatcgggcag caatgtttta tacacggtgc cggcgggtt       1732

acaatcggag aatttgcagg aattggtccg aacgtccgga tacatgccgc ttaccatacc      1792

gatcctgata aacccgacag taccattttg ttttcgccgc ttacattcgc tcctattcat      1852

attgaagaaa actgcaacat cgggatcggt gcgtctatcc tagcaggcgt tacgataggc       1912

gcccactcca aaatcggagc aaatgccgtc gtcaatcgca atattccccc gtacagcata      1972

gca                                                                    1975
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<210> 103

<211>   324

<212>   PRT

<213>   Bacillus licheniformis

<400>   103

Met Ser Asp Met Thr Glu Leu Ser Gly Gln His Ile Phe Ile Thr Gly
1   5   10   15

Gly Ala Gly Phe Ile Gly Ser Ser Leu Ile Gly Lys Leu Ile Glu Arg
            20   25   30

Asn Ser Val Thr Val Tyr Asp Asn Phe Ser Arg Asp Ser Leu Arg Tyr
        35   40   45

Lys Pro Tyr Arg Asp His Pro His Leu Lys Val Leu Gln Gly Asp Ile
    50   55   60

Leu Asp Leu Asn Ala Leu Lys Lys Ala Ile Gln Gly Ala Ser His Ile
65   70   75   80

Val His Ala Ala Gly Ile Ala Gly Ile Asp Thr Val Ile Gln Asn Pro
                85   90   95

Val Lys Thr Met Gln Val Asn Met Ile Gly Ser Ala Asn Leu Leu Glu
                100   105   110

Ala Ala Ala Gly Leu Thr Glu Cys Lys Arg Val Val Cys Phe Ser Thr
            115   120   125

Ser Glu Val Phe Gly Gln Ile Ala Phe Arg Ala Arg Glu Thr Ser His
    130   135   140

Thr Val Leu Gly Ala Val Gly Glu Ala Arg Trp Thr Tyr Ala Val Ser
145   150   155   160

Lys Leu Ala Glu Glu His Met Ala Tyr Ala Tyr Phe Lys Glu Leu Gly
            165   170   175

Leu Pro Thr Val Thr Val Arg Pro Phe Asn Val Tyr Gly Pro Glu Gln
            180   185   190

Val Gly Glu Gly Ala Ile Lys Thr Met Val His Arg Ala Leu Leu Asp
        195   200   205

Glu Pro Ile Tyr Ile His Gly Asp Gly Thr Gln Ile Arg Ala Trp Cys
    210   215   220

Tyr Val Asp Asp Met Ile Asp Gly Ile Leu Arg Cys Leu Thr Met Lys
225   230   235   240

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Glu Ala Ile Gly Glu Ser Phe Asn Ile Gly Asn Glu Arg Thr Val Ile
            245             250             255

Thr Val Tyr Gly Leu Ala Ser Thr Ile Ile Arg Val Leu Gly Ser Lys
            260             265             270

Ser Gln Ile Phe Phe Gly Glu Lys Lys Glu Ala Asp Ile Glu Leu Arg
            275             280             285

Ile Pro Gln Val Asn Lys Ala Lys Glu Met Leu Gly Phe Ser Ala Lys
    290             295             300

Val Asp Leu Glu Glu Gly Ile Arg Arg Thr Ala Glu Ser Ile Lys Lys
305             310             315             320

Asn Leu Asp Gln
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<210> 104

<211> 1213

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(710)

<223>

<400> 104

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acaaactgcg cgaacgccat aacgcgcttg cgatctttac aggggaaagc ctcggccagg      60

tggcaagcca gacgcttgaa agcatgtatg ccatcaacgc ggtcacgagc acgccggttt     120

tgcgcccttt aatcggcatg dataagacgg aaatcatcga aaaagcgaag gaaatcgata     180

cgtacgatat cagcatacgt ccgtacgaag actgctgcac gatctttacg ccttctgcgc     240

cgaaaacgcg tccgaaaaaa gagaaaatcg aacactttga aagctacaca gatttcgaac     300

cgcttatcaa cgaagctgtg gaaaacacgg aaacgattgt tttgagcagc aaagcggaaa     360

cgaaagatca atttgcggat tttttctaaa ggaatattca atcaaacatc tttgtctgtt     420

tttgcataca attaccaaac attctttgta tgaagtcatg tgtttttaca caatctatac     480

tcacaaggag gtgagaacac atg gct caa aac aac aga caa agc agt tct aac     533
                        Met Ala Gln Asn Asn Arg Gln Ser Ser Ser Asn
                         1               5               10

caa cta ttg gtt cct ggt gct gct caa gct atc gac caa atg aaa ttc     581
```

```
Gln Leu Leu Val Pro Gly Ala Ala Gln Ala Ile Asp Gln Met Lys Phe
             15              20              25

gaa atc gct tct gaa ttt ggc gtt aac ctt gga gca gaa act act tct      629
Glu Ile Ala Ser Glu Phe Gly Val Asn Leu Gly Ala Glu Thr Thr Ser
         30              35              40

cgt gca aac ggt tca gtt gga gga gaa atc act aag cgt tta gtt tct      677
Arg Ala Asn Gly Ser Val Gly Gly Glu Ile Thr Lys Arg Leu Val Ser
     45              50              55

ttc gct caa cag caa atg ggt gga aca caa caa taattaaaat taaaaagcaa    730
Phe Ala Gln Gln Gln Met Gly Gly Thr Gln Gln
60              65              70

tggataatgg gtggggttta atccccactc tttttttatgt tctgcaaaat aggcatttcg   790

gaatacaatt gtatgaaagg attatgtata ataaaaagat ggcacaagac aaggagatgg    850

aagggttgag aagagaagat ttgattgcgc cggagaagta taatgcggtt gatgaaattg    910

aaaaatttaa atcttcccgc gataagaccg cattgatctg ggaagatgaa tcagggcgtc    970

aagtgtcatg gtcctatgaa aaattgattg aaaaggctta caaaatcggc agcatattga    1030

cccgttctgg actgaaaaaa ggtgacaagc ttatcgtgat gatgccgcgg ataccggaaa    1090

cgtatgccgt gtacatggcc attttaaaag ctggaatggt ggtcatccca tgttccgaaa    1150

tgcttcgggc gaaagacttg gattacagga tcaagcatgc aggcgtcaaa ggagccgtcg    1210

tat                                                                  1213
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<210> 105

<211> 70

<212> PRT

<213> Bacillus licheniformis

<400> 105

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Met Ala Gln Asn Asn Arg Gln Ser Ser Ser Asn Gln Leu Leu Val Pro
1               5               10              15

Gly Ala Ala Gln Ala Ile Asp Gln Met Lys Phe Glu Ile Ala Ser Glu
             20              25              30

Phe Gly Val Asn Leu Gly Ala Glu Thr Thr Ser Arg Ala Asn Gly Ser
         35              40              45

Val Gly Gly Glu Ile Thr Lys Arg Leu Val Ser Phe Ala Gln Gln Gln
     50              55              60

Met Gly Gly Thr Gln Gln
65              70
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<210> 106

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<211>  1196

<212>  DNA

<213>  Bacillus licheniformis


<220>

<221>  CDS

<222>  (501)..(695)

<223>


<400>  106
cattgtacga gacttaaaat cggtttatga cttcgaaacg atccgtccga tcttaacaac      60

gatttttaat acgattacag accgctccga tgatgtagtg agtccgctgc gcttttatga     120

agggtatgcg cgggtccttg atcatgtgta ccagatcaaa gactatacgc tcaataaatc     180

ggcgcttgaa aaaatcgtca ttgagcagac tggacagctc cgcgattttt ataaagatct     240

ggccgatccc gaatggaaca aagcgagaga catcaccgca gtcactgtgc tgtccgtcat     300

cgcttcgcac attcaggcga ccgcacattc catgattgac agcgtcttct aaaatatga     360

aatgaaataa tcgccgaccg gcgcgcctgg cttgccaatt gccaggcgtt tttttgcct     420

tcaacaattg ccagcataaa aagcctcagt ccaaatcaaa ctaaacaagc agtaccaatt     480

gaaaaaggag ttgagaatgc atg gca aga acg aat aag ctc ctc gtt ccc ggg     533
                         Met Ala Arg Thr Asn Lys Leu Leu Val Pro Gly
                          1               5                  10

gca gag cag gtt tta gac cag ttc aaa tac gaa atc gcc caa gag ttc      581
Ala Glu Gln Val Leu Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe
               15                  20                  25

ggc gtc cag ctc ggc tcg gac tcg gtc gct cgc tca aac gga tct gta     629
Gly Val Gln Leu Gly Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val
               30                  35                  40          .

ggc ggg gaa atg aca aaa cga ctt gta cag cag gca caa gct caa ttg     677
Gly Gly Glu Met Thr Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu
45                  50                  55

aat ggg cat aat gac aaa taaataccct atggattatt cgccgggccc           725
Asn Gly His Asn Asp Lys
60                  65

gctcggcgga tattcttgtt tattcgtttg gtcagaaggc tttttctcct tttggtaagg     785

aagtgattta gagctctctt gatttgaacc ggaaccgctt tttggcgttc cttcctccgt     845

ctgctgaccg tctttgtcat tatggttatg ttcctgaggg ttttttggtat taggggaatt    905

tgactccttt tctttttcca tttcttgatc aggttgagac tgatcttcat ctgaaggttt     965

ttcgccgtcc ggatgatctt ccgtatctgc ttctttatca tccgtatgct gttccggctg    1025

atcttcttct ttcacagctt tctcctttttc tcctgtgttt tcttcctgat tttgatcatc    1085

ttttttatttt tcattgtcat catctttgtt tttgtcttct aattcatctt tgtgggaacg    1145
                         Page 162
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gatataacgg cctgttgaga tgccttcttt ttgggctttt gcacgcgtat c   1196

<210> 107

<211> 65

<212> PRT

<213> Bacillus licheniformis

<400> 107

Met Ala Arg Thr Asn Lys Leu Leu Val Pro Gly Ala Glu Gln Val Leu
1   5   10   15

Asp Gln Phe Lys Tyr Glu Ile Ala Gln Glu Phe Gly Val Gln Leu Gly
                20   25   30

Ser Asp Ser Val Ala Arg Ser Asn Gly Ser Val Gly Gly Glu Met Thr
            35   40   45

Lys Arg Leu Val Gln Gln Ala Gln Ala Gln Leu Asn Gly His Asn Asp
    50   55   60

Lys
65

<210> 108

<211> 2279

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1463)

<223>

<400> 108
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agcggatatt gctgccatta tcaagaaatg caaaaacggc aggagcgaat atatcatcga   120
ccggcttgca ccgaatgaca gcgattattt tttaatcaaa ccaaagcact cagccttta   180
cggcactgct cttgaaacat tgctgcatga acttcatgtc gatcatttga tcatcactgg   240
gatcgcaggc aatatctgcg tattatttac ggcaaacgat gcttatatgc gggagtacga   300
gattacgatt ccgcgcgatt gcatcgcctc aaacaatgaa aaagacaaca aatacgcctt   360
Page 163

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gacgatgatg gaaaatgttc tgttcgccaa tatcacgacg gctaaggcga ttacctccga      420

aacttagagc atgaaacact tcctttcatc atatagtggt agcaatgaga aaggaggcgt      480

ttcccattca gatttatgtc gtg aaa aga ggc gat acc ctt tac caa atc gcg      533
                      Val Lys Arg Gly Asp Thr Leu Tyr Gln Ile Ala
                       1               5                  10

aat cgt tac cga aca aca gtt aat gaa att gtc gcg acg aat gaa att      581
Asn Arg Tyr Arg Thr Thr Val Asn Glu Ile Val Ala Thr Asn Glu Ile
             15                  20                  25

ccg aac ccg aat cgg ctt gtt gtc gga caa acc atc gtg atc ccg atc      629
Pro Asn Pro Asn Arg Leu Val Val Gly Gln Thr Ile Val Ile Pro Ile
         30                  35                  40

gcc ggc gag ttt tat gag gtc aga cag gga gat aca tta gca tca atc      677
Ala Gly Glu Phe Tyr Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile
     45                  50                  55

gga gca cgc ttt aat att tct ccg gct gaa ctg gcg agg atc aac cgc      725
Gly Ala Arg Phe Asn Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg
60                  65                  70                  75

att cag gtt agc gcc gtt tta ccg gtc gga ctg ctg ctt tac atc ccc      773
Ile Gln Val Ser Ala Val Leu Pro Val Gly Leu Leu Leu Tyr Ile Pro
                 80                  85                  90

cct cgg cca aga cgg aac att gaa aca aac gcc tat atc gaa cct cgg      821
Pro Arg Pro Arg Arg Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg
             95                  100                 105

gga gaa agc gta agc ccc gct ttg cag cag gcg gca aga gag gct tcg      869
Gly Glu Ser Val Ser Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser
         110                 115                 120

cca tac ttg acc tat ctg ggc gct ttc agc ttc cag gcg aag cgg gac      917
Pro Tyr Leu Thr Tyr Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp
     125                 130                 135

ggc aca ctc gaa gaa ccg ccg ctg aac aac tta aaa gaa att gcc gac      965
Gly Thr Leu Glu Glu Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp
140                 145                 150                 155

aga cat cgg act acg atg atg atg att gtc acc aat ctc gaa aat gaa      1013
Arg His Arg Thr Thr Met Met Met Ile Val Thr Asn Leu Glu Asn Glu
                 160                 165                 170

gct ttc agc gac gaa ctc ggc agg atc att ctg acg gac cag aat gta      1061
Ala Phe Ser Asp Glu Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val
             175                 180                 185

aaa aac aga ttg ctc gat aac atc gtt gca gcg gcc aga aga tac ggt      1109
Lys Asn Arg Leu Leu Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly
         190                 195                 200

ttt aaa gac atc cat ttt gac ttc gaa tac tta agg ccc gaa gat aga      1157
Phe Lys Asp Ile His Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg
     205                 210                 215

gaa gcc tat aat cag ttt tta cgg gat gcc cgg gcc cgc ttc agg cag      1205
Glu Ala Tyr Asn Gln Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln
220                 225                 230                 235

gaa ggc tgg ctc atc tca acc gcg ctt gct ccg aaa acg aga gcg gat      1253
Glu Gly Trp Leu Ile Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp
             240                 245                 250
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Page 164

```
cag ccc gga caa tgg tat gaa gcc cat gat tac cgg gcc cac ggc gaa    1301
Gln Pro Gly Gln Trp Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu
            255                 260                 265

att gtc gat ttc gtc gtg ctg atg aca tat gag tgg ggc tac agc gga    1349
Ile Val Asp Phe Val Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly
            270                 275                 280

ggg ccc ccg atg gcg gta tcg ccg. atc ggg ccc gtc cgg gac gtg atc   1397
Gly Pro Pro Met Ala Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile
            285                 290                 295

gaa tac gca ctc acg gaa atg ccc gcc agc aaa atc gtc atg gga cag    1445
Glu Tyr Ala Leu Thr Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln
300                 305                 310                 315

aaa ctg tac ggc tat gac tgacgctccc ctatatgcac agcgggaccc           1493
Lys Leu Tyr Gly Tyr Asp
            320

gttggccaag accaatccgg ccccaacggg gggattgaga tcgcgagcga gaacaatgcg  1553

gcgatacagt acgatgaaac agctcaggct ccaaacttcc gctatacgga caatgccggc  1613

aaacagcatg aagtatggtt tgaagacgcc cgctcgattc aggcaaagtt tgatctgatt  1673

agggaattga atttaagggg aatcagctat tggaagctcg gcctgtcctt cccgcaaaac  1733

tggctcttga tagccgatca atttaatgtt gttaaagaga cgttcccaag ttaaaggaac  1793

gttttttttc atggcagcgg atgatgatgt gatacaatat gtatggttca caaatgaatt  1853

tctttagtag gaggacacct atgaatacag ccccttttcat tgctgtcgaa ggccccatcg  1913

gcgcgggaaa aacaaccttg gccagcatgc tctccgaaaa gctctcactc tctttggtca  1973

aagaaatcgt cgaagaaaac ccttttcttg ataaatttta tgatgaaaaa gatgaatgga  2033

gctttcagct tgagatgttt ttcctctgca atcgctataa gcagcttgaa gataccgaga  2093

aaaagtattt gcatcatcac atgcccgttg tttcggacta tcatatttat aaaaacctca  2153

tttttgccga acggacgctg gaaggcaaaa aacttgagaa atacagaaaa atttatcagc  2213

tgcttacaga agatctgccg aaaccaaacg tcatcattta cataagagcg agtcttccaa  2273

ctttat                                                             2279
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<210> 109

<211> 321

<212> PRT

<213> Bacillus licheniformis

<400> 109

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Val Lys Arg Gly Asp Thr Leu Tyr Gln Ile Ala Asn Arg Tyr Arg Thr
1               5                 10                  15

Thr Val Asn Glu Ile Val Ala Thr Asn Glu Ile Pro Asn Pro Asn Arg
            20                  25                  30
```

Leu Val Val Gly Gln Thr Ile Val Ile Pro Ile Ala Gly Glu Phe Tyr
        35   40   45

Glu Val Arg Gln Gly Asp Thr Leu Ala Ser Ile Gly Ala Arg Phe Asn
        50   55   60

Ile Ser Pro Ala Glu Leu Ala Arg Ile Asn Arg Ile Gln Val Ser Ala
65   70   75   80

Val Leu Pro Val Gly Leu Leu Leu Tyr Ile Pro Pro Arg Pro Arg Arg
                85   90   95

Asn Ile Glu Thr Asn Ala Tyr Ile Glu Pro Arg Gly Glu Ser Val Ser
            100   105   110

Pro Ala Leu Gln Gln Ala Ala Arg Glu Ala Ser Pro Tyr Leu Thr Tyr
        115   120   125

Leu Gly Ala Phe Ser Phe Gln Ala Lys Arg Asp Gly Thr Leu Glu Glu
    130   135   140

Pro Pro Leu Asn Asn Leu Lys Glu Ile Ala Asp Arg His Arg Thr Thr
145   150   155   160

Met Met Met Ile Val Thr Asn Leu Glu Asn Glu Ala Phe Ser Asp Glu
            165   170   175

Leu Gly Arg Ile Ile Leu Thr Asp Gln Asn Val Lys Asn Arg Leu Leu
        180   185   190

Asp Asn Ile Val Ala Ala Ala Arg Arg Tyr Gly Phe Lys Asp Ile His
        195   200   205

Phe Asp Phe Glu Tyr Leu Arg Pro Glu Asp Arg Glu Ala Tyr Asn Gln
210   215   220

Phe Leu Arg Asp Ala Arg Ala Arg Phe Arg Gln Glu Gly Trp Leu Ile
225   230   235   240

Ser Thr Ala Leu Ala Pro Lys Thr Arg Ala Asp Gln Pro Gly Gln Trp
            245   250   255

Tyr Glu Ala His Asp Tyr Arg Ala His Gly Glu Ile Val Asp Phe Val
            260   265   270

Val Leu Met Thr Tyr Glu Trp Gly Tyr Ser Gly Gly Pro Pro Met Ala
    275   280   285

Val Ser Pro Ile Gly Pro Val Arg Asp Val Ile Glu Tyr Ala Leu Thr
290   295   300

Page 166

```
Glu Met Pro Ala Ser Lys Ile Val Met Gly Gln Lys Leu Tyr Gly Tyr
305                 310             315                 320

Asp


<210>   110

<211>   2011

<212>   DNA

<213>   Bacillus licheniformis


<220>

<221>   CDS

<222>   (252)..(1508)

<223>


<400>   110
gaattggccg aaaacctcca tcgctttatg aaggacgaga gcggtatcaa attctttgct     60

ccttcccaag cccctatcac ctcctttatt tgaaggatac actttctaga ctgttcagtc    120

aagaattatc cgcttcacgg ttctattcac cattccagct gtaaaaaacg gcgcatgatc    180

cttctgcaac ggtcatagac atagcataaa accccctgtc acatacagag gaacaaaagg    240

aagtgtgcca g ttg ttt att tat aca gtc cag ccg gga gat tca cta ttt    290
           Leu Phe Ile Tyr Thr Val Gln Pro Gly Asp Ser Leu Phe
            1               5                  10

gtc atc ggc gcc aag ttc gga att tcg att gac cag atc cga ttg gcg    338
Val Ile Gly Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala
         15               20              25

aat ggg ttg atc gca aca aac att gtc ccc gga cag gct ctt tta ata    386
Asn Gly Leu Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile
30               35              40              45

ccg ctt tat aca tat acc gtt cag ccg gga gac agt tat tac acg att    434
Pro Leu Tyr Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile
             50              55              60

gcc cgc cgg acg ttt gta tcc gtc gaa gca ttg caa aaa gca aat ccg    482
Ala Arg Arg Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro
             65              70              75

tct gta acc cct tcc aat atg agg ccg ggg ata aaa gtg atg att ccg    530
Ser Val Thr Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro
         80              85              90

gaa ttg ccg aaa aaa ccg atc act gct tta gga tat tac aca ctg aga    578
Glu Leu Pro Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg
     95              100             105

aac ccc cgg tta gac cag gaa ttg att cat aat ttt gcc cca tac gcc    626
                          Page 167
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```
Asn Pro Arg Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala
110             115             120             125

acg tat ctg gca ttt ttt gaa tac cac att tca agc gac gga tcg tta    674
Thr Tyr Leu Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu
            130             135             140

agc gag ctg aat gat tca ccg gcc gta caa acg gct tgg aga cgg cgc    722
Ser Glu Leu Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg
            145             150             155

gtt cct ccc ctc atg aca gtc acc aat cta act gaa tca ggc ttc agt    770
Val Pro Pro Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser
    160             165             170

ccg tct ctt gcg cac cgc gta tta aat cag cct gcc gta aga aat cgc    818
Pro Ser Leu Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg
    175             180             185

ctc atc gac aat att gtc caa acg att tcc aga aaa gga tat gca ggc    866
Leu Ile Asp Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly
190             195             200             205

gtc aat att gat ttc gaa cag att ttg gag gaa gac aga gat tta ttt    914
Val Asn Ile Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe
            210             215             220

tca ggt ttt ctc cgc ctg ttg aaa gag cgg ctg aag ccg tcc ggc tat    962
Ser Gly Phe Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr
            225             230             235

gtg ttg acg att gcc gtt ccg ccg aaa aca aat gaa aat atc gcc tgg    1010
Val Leu Thr Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp
            240             245             250

ctg aaa ggg tat gac tat ggc gga atc ggt gca gtg agc gac ctt atc    1058
Leu Lys Gly Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile
    255             260             265

ttc atc atg gca tac gac tgg cac cac ggg aca agc gag ccc ggc ccc    1106
Phe Ile Met Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro
270             275             280             285

att gct ccg atc aat gaa gtc cgg caa aca att caa ttt gct ctc cgc    1154
Ile Ala Pro Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg
            290             295             300

cat gtc ccc aaa gaa aaa atc gtt ctc ggc ttt ccg ctt tac ggc tat    1202
His Val Pro Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr
            305             310             315

aac tgg acc ctg ccc tat cag ccc ggt gcc gta tac ccc gga atc gcc    1250
Asn Trp Thr Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala
            320             325             330

aac caa gac gcc gtt cag ctc gcc atg aag cac cag gca ccg att caa    1298
Asn Gln Asp Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln
            335             340             345

tat gat aca aat tct gag tcc cct ttt ttc aga tac acc gat gaa cag    1346
Tyr Asp Thr Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln
350             355             360             365

ggc aga cgg cat gtc gta tgg ttt gaa gac gca cgc agc atc gga aaa    1394
Gly Arg Arg His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys
            370             375             380

aaa ctg cag ctg atc acc gaa tac gga ctt gac ggc ggc ggc gtc tgg    1442
```

Page 168

```
Lys Leu Gln Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Gly Val Trp
            385               390               395

cag ctc aca ctc agt ttt ccg caa gga aca tgg ctc ttg acc aaa ttc    1490
Gln Leu Thr Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe
            400               405               410

ttt cgc gtc cga aaa gtc tgacatcatt atgtgattta ttgtaaaata          1538
Phe Arg Val Arg Lys Val
            415

acaaaccgaa taatcccgct aacgaatttt gatactaaag atgtgtcctt cacacaataa   1598

caaatttgaa aggaatgttt gcgattgaat aatgcgatcc atgaaacatt ggagctgcat   1658

gagctgttaa tgtttaaaaa cctttgtctg acaaagtcat caacaatgac gggaatggtt   1718

caggatcaag agcttcgcga catcttggag cgtgatgcat cccaaacaaa gcatcagatc   1778

gagcatttac aaggtctatt gtcagtgaga ggtgaaaccg tatgaacgaa ttcatccaaa   1838

acatgacagg catgggcgcg atgactgaac aagtcattgc caccgatttt ttaatctcgg   1898

caaaaaccgg tgtcaaaaac attgccacag ctatcacgga aacatcttct ccagaagtgc   1958

gcgaaacgct taagcagtat ttaaacgacg cgattgacac ccatgaacag atc         2011
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<210> 111

<211> 419

<212> PRT

<213> Bacillus licheniformis

<400> 111

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Leu Phe Ile Tyr Thr Val Gln Pro Gly Asp Ser Leu Phe Val Ile Gly
1               5               10              15


Ala Lys Phe Gly Ile Ser Ile Asp Gln Ile Arg Leu Ala Asn Gly Leu
            20              25              30


Ile Ala Thr Asn Ile Val Pro Gly Gln Ala Leu Leu Ile Pro Leu Tyr
        35              40              45


Thr Tyr Thr Val Gln Pro Gly Asp Ser Tyr Tyr Thr Ile Ala Arg Arg
    50              55              60


Thr Phe Val Ser Val Glu Ala Leu Gln Lys Ala Asn Pro Ser Val Thr
 65              70              75              80


Pro Ser Asn Met Arg Pro Gly Ile Lys Val Met Ile Pro Glu Leu Pro
            85              90              95


Lys Lys Pro Ile Thr Ala Leu Gly Tyr Tyr Thr Leu Arg Asn Pro Arg
            100             105             110
```

Page 169

Leu Asp Gln Glu Leu Ile His Asn Phe Ala Pro Tyr Ala Thr Tyr Leu
   115   120   125

Ala Phe Phe Glu Tyr His Ile Ser Ser Asp Gly Ser Leu Ser Glu Leu
  130   135   140

Asn Asp Ser Pro Ala Val Gln Thr Ala Trp Arg Arg Arg Val Pro Pro
145   150   155   160

Leu Met Thr Val Thr Asn Leu Thr Glu Ser Gly Phe Ser Pro Ser Leu
     165   170   175

Ala His Arg Val Leu Asn Gln Pro Ala Val Arg Asn Arg Leu Ile Asp
    180   185   190

Asn Ile Val Gln Thr Ile Ser Arg Lys Gly Tyr Ala Gly Val Asn Ile
   195   200   205

Asp Phe Glu Gln Ile Leu Glu Glu Asp Arg Asp Leu Phe Ser Gly Phe
  210   215   220

Leu Arg Leu Leu Lys Glu Arg Leu Lys Pro Ser Gly Tyr Val Leu Thr
225   230   235   240

Ile Ala Val Pro Pro Lys Thr Asn Glu Asn Ile Ala Trp Leu Lys Gly
     245   250   255

Tyr Asp Tyr Gly Gly Ile Gly Ala Val Ser Asp Leu Ile Phe Ile Met
   260   265   270

Ala Tyr Asp Trp His His Gly Thr Ser Glu Pro Gly Pro Ile Ala Pro
  275   280   285

Ile Asn Glu Val Arg Gln Thr Ile Gln Phe Ala Leu Arg His Val Pro
  290   295   300

Lys Glu Lys Ile Val Leu Gly Phe Pro Leu Tyr Gly Tyr Asn Trp Thr
305   310   315   320

Leu Pro Tyr Gln Pro Gly Ala Val Tyr Pro Gly Ile Ala Asn Gln Asp
    325   330   335

Ala Val Gln Leu Ala Met Lys His Gln Ala Pro Ile Gln Tyr Asp Thr
   340   345   350

Asn Ser Glu Ser Pro Phe Phe Arg Tyr Thr Asp Glu Gln Gly Arg Arg
  355   360   365

His Val Val Trp Phe Glu Asp Ala Arg Ser Ile Gly Lys Lys Leu Gln
  370   375   380

Page 170

```
Leu Ile Thr Glu Tyr Gly Leu Asp Gly Gly Gly Val Trp Gln Leu Thr
385             390             395             400
```

```
Leu Ser Phe Pro Gln Gly Thr Trp Leu Leu Thr Lys Phe Phe Arg Val
                405             410             415
```

```
Arg Lys Val
```

<210> 112

<211> 2014

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (558)..(1511)

<223>

<400> 112

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tggtagacgg caacaagcgg ctgcgccctt ccgtctgcga caggcacgac ggcgtcatcc        60

gccggggtca actgccgttt taaagccgat atggtctcct gccggacaag cggggtgtca       120

catggccgaa aaaatatagc attcccttc cgcccgctcc atggctgtgt acataccggc        180

aagcggccct ttccctctgt acgggtcgat atcttccagc accgctttt tcccgagttc        240

tataaaccgc tccgtcaagc ccggacggct caatatcagg acgtcgtctc ccagcgcctg       300

tttgcaccat tgataaagcg gcttgccttt ccagcgggca aacgccttcg gttccccaaa       360

acggcgcgaa agccccctg ataatatgac atgtatttct ttcatacggc tcaaccttcc        420

ttcgcgtgtt cctgcctgcg aacatcatag caaaacttta gaaatccgaa caagtctgta       480

aaatctcttt ttcaaaaggc atggcgggtt tcatttatgc atattgtagt tgtaacattt       540
```

```
ataggggggct ggtcacc atg aaa aaa aca tcg ggt tcg ctg cct tat ttt        590
                    Met Lys Lys Thr Ser Gly Ser Leu Pro Tyr Phe
                    1             5                   10
```

```
caa gat tta tca cag gaa aac ctt ttt tta aaa gct gag ctg gca aga        638
Gln Asp Leu Ser Gln Glu Asn Leu Phe Leu Lys Ala Glu Leu Ala Arg
            15                  20                  25
```

```
tca cat caa ttg ata cac gag ctt gaa gca agc tat ttt cac cag aaa        686
Ser His Gln Leu Ile His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys
        30                  35                  40
```

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aat cat aag ctc agc cgg gaa aac gca gca atg aaa cag cag ctt cag        734
Asn His Lys Leu Ser Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln
    45                  50                  55
```

```
cag ctg tca ttc gaa ctg gag cgg att tcg gca aac aag gaa gac aag        782
```

```
Gln Leu Ser Phe Glu Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys
60              65          70              75

tcg gcc gaa acg ctc aac cgg ata aaa agc gaa ttg ctg agt aaa atc    830
Ser Ala Glu Thr Leu Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile
             80              85              90

gtc gtt ctt cag gag ctt ctt caa aaa gaa acc tat gca aga aaa caa    878
Val Val Leu Gln Glu Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln
             95              100             105

gag ata gaa gaa aag cac cgc ctt cat tta aca aat gta aaa gcc gaa    926
Glu Ile Glu Glu Lys His Arg Leu His Leu Thr Asn Val Lys Ala Glu
         110             115             120

gaa gag aaa aaa agc tta cat agc caa ata gaa tac gaa aag ctt cat    974
Glu Glu Lys Lys Ser Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His
125             130             135

gca gaa aga gaa aaa acg ctg agg gaa aaa aag gaa cag gag ctc aaa    1022
Ala Glu Arg Glu Lys Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys
140             145             150             155

aac gct gca tac gaa aat gcc cgc ctg aaa gat gaa ctt cat gct aaa    1070
Asn Ala Ala Tyr Glu Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys
             160             165             170

agt ctt cag ctc aaa caa atc gaa act gat gtt gcg gta tta aaa gag    1118
Ser Leu Gln Leu Lys Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu
             175             180             185

cgg gtg acg gaa acg aaa agc cgg ctt ttg gag gct gaa aaa aca aaa    1166
Arg Val Thr Glu Thr Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys
             190             195             200

gaa gcg ctg ttt tat gaa acg att ctc tct tat aaa agg caa ctc gat    1214
Glu Ala Leu Phe Tyr Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp
205             210             215

gaa agt gat aag tgg atc gct tct cat ttt gcc gat att gat gca ttt    1262
Glu Ser Asp Lys Trp Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe
220             225             230             235

cag cag acg gag aag gcg ctt gaa caa aac gag gag gtt ttt gaa cgg    1310
Gln Gln Thr Glu Lys Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg
             240             245             250

aca gaa cag atc gag gcg gtg ctt caa act gtt aca gag caa gtt gat    1358
Thr Glu Gln Ile Glu Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp
             255             260             265

cag ctc caa caa caa ttg agc gcc att caa caa aat tat acg aaa atg    1406
Gln Leu Gln Gln Gln Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met
             270             275             280

gat caa aaa ata aca gaa tgg aaa aaa cag gcg aaa gaa gaa aca ccc    1454
Asp Gln Lys Ile Thr Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro
285             290             295

ccg caa aaa tgg gtc tat caa att aaa cgc aaa gac aaa gaa aca aaa    1502
Pro Gln Lys Trp Val Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys
300             305             310             315

cct tta aat taaataccac tttaaggaat aatttggttt ttacaaaaaa          1551
Pro Leu Asn

accgcttgag tagattgtct caagcagttg attgggcggc ggcgtataaa gcggccgcct   1611
```

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ttatgttccc ttaaaatgga aacgctatct gaaaaagcaa gggtttgacc tattgctgct   1671

ctgtctcagt agaaatctca ccctctaata tatattgacc gcggtatggt tttttgactt   1731

ccgggtacat tttaatcagg ctttgcataa aggttgtcat attagggatc tcaagtccgc   1791

tctctttttc gatttctttt tgaagttcgg agcttttgat ggccgcatta tggcgtttta   1851

atgttttaat cgccgcttca cgcaattttg cagcttttga gcctggacgt gctgtacccc   1911

ttctgcgcct tgtcgttcca tctggaattc cggcaggcag tgaggaggtt tgcggagaag   1971

tctgctgctg gttcttttga gatgcttgcg gctgctgttg ctg                     2014
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<210> 113

<211> 318

<212> PRT

<213> Bacillus licheniformis

<400> 113

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Met Lys Lys Thr Ser Gly Ser Leu Pro Tyr Phe Gln Asp Leu Ser Gln
1               5               10              15


Glu Asn Leu Phe Leu Lys Ala Glu Leu Ala Arg Ser His Gln Leu Ile
            20              25              30


His Glu Leu Glu Ala Ser Tyr Phe His Gln Lys Asn His Lys Leu Ser
        35              40              45


Arg Glu Asn Ala Ala Met Lys Gln Gln Leu Gln Gln Leu Ser Phe Glu
    50              55              60


Leu Glu Arg Ile Ser Ala Asn Lys Glu Asp Lys Ser Ala Glu Thr Leu
65              70              75              80


Asn Arg Ile Lys Ser Glu Leu Leu Ser Lys Ile Val Val Leu Gln Glu
            85              90              95


Leu Leu Gln Lys Glu Thr Tyr Ala Arg Lys Gln Glu Ile Glu Glu Lys
            100             105             110


His Arg Leu His Leu Thr Asn Val Lys Ala Glu Glu Glu Lys Lys Ser
            115             120             125


Leu His Ser Gln Ile Glu Tyr Glu Lys Leu His Ala Glu Arg Glu Lys
    130             135             140


Thr Leu Arg Glu Lys Lys Glu Gln Glu Leu Lys Asn Ala Ala Tyr Glu
145             150             155             160
```

Page 173

```
Asn Ala Arg Leu Lys Asp Glu Leu His Ala Lys Ser Leu Gln Leu Lys
            165             170             175

Gln Ile Glu Thr Asp Val Ala Val Leu Lys Glu Arg Val Thr Glu Thr
            180             185             190

Lys Ser Arg Leu Leu Glu Ala Glu Lys Thr Lys Glu Ala Leu Phe Tyr
            195             200             205

Glu Thr Ile Leu Ser Tyr Lys Arg Gln Leu Asp Glu Ser Asp Lys Trp
    210             215             220

Ile Ala Ser His Phe Ala Asp Ile Asp Ala Phe Gln Gln Thr Glu Lys
225             230             235             240

Ala Leu Glu Gln Asn Glu Glu Val Phe Glu Arg Thr Glu Gln Ile Glu
            245             250             255

Ala Val Leu Gln Thr Val Thr Glu Gln Val Asp Gln Leu Gln Gln Gln
            260             265             270

Leu Ser Ala Ile Gln Gln Asn Tyr Thr Lys Met Asp Gln Lys Ile Thr
            275             280             285

Glu Trp Lys Lys Gln Ala Lys Glu Glu Thr Pro Pro Gln Lys Trp Val
    290             295             300

Tyr Gln Ile Lys Arg Lys Asp Lys Glu Thr Lys Pro Leu Asn
305             310             315
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<210> 114

<211> 2341

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1838)

<223>

<400> 114

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tgaaagacag ccgatttcct gacagcgtaa aaagcgtgat ctatcaaaga aacgcttttg     120
agcccgttct aaacggcagc atcgagaaaa aagcagaccg cgaatcagtg gaagctgtgg     180
aagaagcggt agatcaaaat aaaaaagaaa cagaagcttt atttttctat aatcccgaca     240
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tcgcttctga tgactggatt aaaacgagaa aagtcgtgaa gcgcatcggc aatcatgtct      300

ttgcgatcta gaaagcagtc agggccattc gccttggctg ctttttttgt gcgattcttt      360

cttacgcatt atcatctttc acagcccaag aaaaaattta tttttgatac tttatgaaaa      420

tcaattttca attaaaaaga aaataatttt tagacttgtc tcatatgatg ggataaaccc      480

gtgagacaag gagagacctc atg aac cgt ttt gta aaa gga atc gtt ctt ctt      533
                        Met Asn Arg Phe Val Lys Gly Ile Val Leu Leu
                         1               5                  10

tcg cta gct gct ttt ttt gca gaa tgt ctt gaa ttc gtc atc aac atg      581
Ser Leu Ala Ala Phe Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met
            15              20                  25

att ctt gca cgg gag ctt ggc gag cat ggc atg ggg ctc tac atg agt      629
Ile Leu Ala Arg Glu Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser
        30                  35                  40

gtt ttg cct tcc att ttt ttg gtc gtg gtg att gcg agc ctt gag ctg      677
Val Leu Pro Ser Ile Phe Leu Val Val Val Ile Ala Ser Leu Glu Leu
        45              50                  55

ccc gta tca ata tcg aag ttt atc gcc gag tcc aac ccg aag ctg cac      725
Pro Val Ser Ile Ser Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His
60              65                  70                  75

gaa agc atg ctg aaa cat gca ttg cgg atg act gcg gtc tgc acg gtt      773
Glu Ser Met Leu Lys His Ala Leu Arg Met Thr Ala Val Cys Thr Val
                80                  85                  90

ttc tcc acg gca gcc gca gtg atc att ctt cca ttt att ccg gtt ttt      821
Phe Ser Thr Ala Ala Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe
                95                  100                 105

gat tct tac cac cct cta atc aga gga ctt gtg atc ggg atg att cct      869
Asp Ser Tyr His Pro Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro
            110                 115                 120

acg gtt gca ttc aca tcg atc gcg aga ggc tac ttc atg ggc gtt cag      917
Thr Val Ala Phe Thr Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln
        125                 130                 135

caa atg ggt aaa atc gca acg gcg aat gcc ttg aaa aaa atc ttt cag      965
Gln Met Gly Lys Ile Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln
140                 145                 150                 155

ctc atc ggc ttg ttt tta ttt ttt caa tgg tat tcc ttt gaa ttg gat     1013
Leu Ile Gly Leu Phe Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp
                160                 165                 170

act tct ctt ctc att tca ttg ttt gtc ctc gtt gca agt gaa gtg gtc     1061
Thr Ser Leu Leu Ile Ser Leu Phe Val Leu Val Ala Ser Glu Val Val
            175                 180                 185

gtg ttt gtt tat ttg ttt tcg cag ttt gtt ttg gtc agg cgt gcc gct     1109
Val Phe Val Tyr Leu Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala
        190                 195                 200

caa aaa ggg cag cag atc cac ttg cgg aga aac gat gtt tta aaa cgc     1157
Gln Lys Gly Gln Gln Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg
205                 210                 215

ctg ctc act gtt tcg atc ccg acg acg ggg ctg cgc gtg ttt cat gct     1205
Leu Leu Thr Val Ser Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala
220                 225                 230                 235
```

Page 175

```
gtg aca aat gcc gtc gaa cct ttt ttg gtg aag ggg acg ctg ctt gcc    1253
Val Thr Asn Ala Val Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala
            240              245              250

gct ggc gta tca aga aca tcg gcc atc gac cag ttc ggc atg ctt tcg    1301
Ala Gly Val Ser Arg Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser
            255              260              265

gga gtt gcg atg aca atc ggc ttt ttt ccg gct ttt atc gcc cat tca    1349
Gly Val Ala Met Thr Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser
            270              275              280

ctg atg gtc gtc atg atc ccg agc att tct gaa agc tac gct tac ggg    1397
Leu Met Val Val Met Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly
            285              290              295

caa tac gaa aga gtg atc aaa cgg att aaa cag gcg atc ttt att acg    1445
Gln Tyr Glu Arg Val Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr
300              305              310              315

ctg ttt tac ggc ata ccg tcc gtc atg gtg atg tat cac ttt gca gag    1493
Leu Phe Tyr Gly Ile Pro Ser Val Met Val Met Tyr His Phe Ala Glu
                320              325              330

ccg ctg acc cat tta ttt ttc gat tcg gtc aag gcg tcg ttt tac ctt    1541
Pro Leu Thr His Leu Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu
                335              340              345

aaa atg ttg tgg ccg tat ttt tta ttc cac ttt ttt gcg atg cct ttt    1589
Lys Met Leu Trp Pro Tyr Phe Leu Phe His Phe Phe Ala Met Pro Phe
                350              355              360

cag gcc tgt tta atc gga atg ggg ttg gcc aaa gat gct ttt tat cat    1637
Gln Ala Cys Leu Ile Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His
                365              370              375

aac gtt tgg gcc agt gtc tta tcg ttt ttg atg atg tat gtt ctc ggg    1685
Asn Val Trp Ala Ser Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly
380              385              390              395

tcc atg cag act ttg cag atg acg ggg atc att ctt gcg atg aat acc    1733
Ser Met Gln Thr Leu Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr
                400              405              410

ggt atg att ttg ctg acg gcg ctg cat tat gtg acg att tgc aag gag    1781
Gly Met Ile Leu Leu Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu
                415              420              425

ctg ggc gtc acg ctt ttt ttg aca aac aaa tcc cga tct ccg aga att    1829
Leu Gly Val Thr Leu Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile
                430              435              440

gaa agc cgc tgatggatcc tcttcatagt tttagctttt gcggggaagc            1878
Glu Ser Arg
                445

taatattaaa aaagaagggg agttcccatg cgaagaatca gtctcattta cccgctcatc  1938

ctgctgtttt ttaccgggtt attcgtattt cagccgcagg catctgcaaa acaagcttcg  1998

ccggcagtca tgcagatgaa cacggtcgaa ggtcagcgcg tcgtcattcc cgccgaaggc  2058

cagaagacga tcgttcattt ttggacgacc tggtgcccgc catgccgtga agagcttccg  2118

cgattccaat cctactatga aagcaagcaa tccggcgtca agctcgtgac cgttaattta  2178

ctgaatgccg aaaagaacga acagaaggta aaacagttta ttaaagcaaa caagctgaca  2238
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tttccgatcg tttttgacaa aaagggtgag atgatgaaag catataaagt catgacaatt   2298

cctacgactt ttttctttaa tgaaaaagga gagctggaga aaa   2341

<210>   115

<211>   446

<212>   PRT

<213>   Bacillus licheniformis

<400>   115

Met Asn Arg Phe Val Lys Gly Ile Val Leu Leu Ser Leu Ala Ala Phe
1   5   10   15

Phe Ala Glu Cys Leu Glu Phe Val Ile Asn Met Ile Leu Ala Arg Glu
                20   25   30

Leu Gly Glu His Gly Met Gly Leu Tyr Met Ser Val Leu Pro Ser Ile
            35   40   45

Phe Leu Val Val Val Ile Ala Ser Leu Glu Leu Pro Val Ser Ile Ser
    50   55   60

Lys Phe Ile Ala Glu Ser Asn Pro Lys Leu His Glu Ser Met Leu Lys
65   70   75   80

His Ala Leu Arg Met Thr Ala Val Cys Thr Val Phe Ser Thr Ala Ala
                85   90   95

Ala Val Ile Ile Leu Pro Phe Ile Pro Val Phe Asp Ser Tyr His Pro
                100   105   110

Leu Ile Arg Gly Leu Val Ile Gly Met Ile Pro Thr Val Ala Phe Thr
            115   120   125

Ser Ile Ala Arg Gly Tyr Phe Met Gly Val Gln Gln Met Gly Lys Ile
    130   135   140

Ala Thr Ala Asn Ala Leu Lys Lys Ile Phe Gln Leu Ile Gly Leu Phe
145   150   155   160

Leu Phe Phe Gln Trp Tyr Ser Phe Glu Leu Asp Thr Ser Leu Leu Ile
                165   170   175

Ser Leu Phe Val Leu Val Ala Ser Glu Val Val Val Phe Val Tyr Leu
                180   185   190

Phe Ser Gln Phe Val Leu Val Arg Arg Ala Ala Gln Lys Gly Gln Gln
            195   200   205

```
Ile His Leu Arg Arg Asn Asp Val Leu Lys Arg Leu Leu Thr Val Ser
210             215         220

Ile Pro Thr Thr Gly Leu Arg Val Phe His Ala Val Thr Asn Ala Val
225             230         235             240

Glu Pro Phe Leu Val Lys Gly Thr Leu Leu Ala Ala Gly Val Ser Arg
                245         250             255

Thr Ser Ala Ile Asp Gln Phe Gly Met Leu Ser Gly Val Ala Met Thr
                260         265             270

Ile Gly Phe Phe Pro Ala Phe Ile Ala His Ser Leu Met Val Val Met
                275         280         285

Ile Pro Ser Ile Ser Glu Ser Tyr Ala Tyr Gly Gln Tyr Glu Arg Val
        290         295         300

Ile Lys Arg Ile Lys Gln Ala Ile Phe Ile Thr Leu Phe Tyr Gly Ile
305             310         315             320

Pro Ser Val Met Val Met Tyr His Phe Ala Glu Pro Leu Thr His Leu
                325         330             335

Phe Phe Asp Ser Val Lys Ala Ser Phe Tyr Leu Lys Met Leu Trp Pro
                340         345             350

Tyr Phe Leu Phe His Phe Phe Ala Met Pro Phe Gln Ala Cys Leu Ile
            355         360             365

Gly Met Gly Leu Ala Lys Asp Ala Phe Tyr His Asn Val Trp Ala Ser
    370             375         380

Val Leu Ser Phe Leu Met Met Tyr Val Leu Gly Ser Met Gln Thr Leu
385             390         395             400

Gln Met Thr Gly Ile Ile Leu Ala Met Asn Thr Gly Met Ile Leu Leu
                405         410             415

Thr Ala Leu His Tyr Val Thr Ile Cys Lys Glu Leu Gly Val Thr Leu
                420         425             430

Phe Leu Thr Asn Lys Ser Arg Ser Pro Arg Ile Glu Ser Arg
        435             440         445
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<210> 116

<211> 1417

<212> DNA

<213>   Bacillus licheniformis

<220>

<221>   CDS

<222>   (420)..(914)

<223>

<400>   116
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tgaggtgaca atcggaatgc ccgcctggtt gatcgcctca atatcccgat aaatcgttct   120

gacagagact tcgaacatgc cggcaagctc ctttgcctgc acttggcgtt tattaatcaa   180

taaaatcaca atggccaaaa gccggtcaat tttcactgca gatccctcac attcatcttg   240

tgcagcctct ttttttctgc tattttcatt ccatagcgca caccattctg ggatatcatg   300

acaaaaaaga ggatctcatc acccatttat ctagaaaacc acttttcagg ttacgatttg   360

tacagtttgg acatatactc cttaaaaaag gaggttttaa aaacatcata ttttatttt   419

ttg cag ttt ttc atc att gtg tcc atc gtc tat atc aag ttc aaa cgg   467
Leu Gln Phe Phe Ile Ile Val Ser Ile Val Tyr Ile Lys Phe Lys Arg
1   5   10   15

tcg gtc ggt tat cag cct tta aag ccg gca cgc atg ttg ttc cgg atc   515
Ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile
            20   25   30

atc ctt ttt tcg gga att ttc gtt ttt ctg ctg acg atg agc gca ctt   563
Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu
        35   40   45

cac cct tta tca tac ttt tat gat ctg att ggg atc gcg ctc gga ctc   611
His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu
50   55   60

atc ttg acc gtc tat gcg ctg aag cat gtg tcg atc gaa aat cgg ggc   659
Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly
65   70   75   80

gga gtc ctt tat ttc aga acg cat tta tgg gtt gaa ttg atc gta ctc   707
Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu
                85   90   95

ttt tta ttt tta tac cgg ttt ctg tac cgg atc gcc gag atc ggc cag   755
Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln
            100   105   110

ctg cag act gcg gtt tca gac ggg ggt tcg gca gct tac ggc gcc ctt   803
Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu
            115   120   125

ttt gcg cag gac ccg gcg acg atg atc ggt ttt ttt gta ctg gcc gtt   851
Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val
130   135   140

tat tat gtc ggt ttc tct ttt ttt gtt tta aaa aaa ggc aga acc gaa   899
Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu
145   150   155   160

Page 179

```
gaa aag cgc tca gct taaaaaggca aactcgggaa attgagtttg ccttttaaac        954
Glu Lys Arg Ser Ala
              165

tttagtcatg ttgtgtatga tcgatcatct gctgaagtac atcgaggaca tgctggtctt       1014

ccggagaata aaaaatggaa gtccctgccc ttcttgattt gacgagacga aggttttta        1074

aaaacctgag ctggtgagaa acggttgact gcaggagact cagcttctct gctatttcat       1134

taaccgaatg ctcgccttgt gagagcaggt gaagaatttt gattctcgtt gggtcagaga       1194

gcgctttaaa cgtctgtgaa acgagaaata aagtttcttc atctaactcg gcccgcacct       1254

gtttttctgt tgtttcttga ttgtgctcac tcatgctttt cacctttcc gcgcgacttt        1314

tacctccata tcatatacca aaacataccg gttgaaaagt tttaacggat caagtcgaaa       1374

acagcgttcc ttgaagcgct tctacatatc ttgcagcaga cct                         1417
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<210> 117

<211> 165

<212> PRT

<213> Bacillus licheniformis

<400> 117

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Leu Gln Phe Phe Ile Ile Val Ser Ile Val Tyr Ile Lys Phe Lys Arg
1               5               10              15

Ser Val Gly Tyr Gln Pro Leu Lys Pro Ala Arg Met Leu Phe Arg Ile
            20              25              30

Ile Leu Phe Ser Gly Ile Phe Val Phe Leu Leu Thr Met Ser Ala Leu
        35              40              45

His Pro Leu Ser Tyr Phe Tyr Asp Leu Ile Gly Ile Ala Leu Gly Leu
    50              55              60

Ile Leu Thr Val Tyr Ala Leu Lys His Val Ser Ile Glu Asn Arg Gly
65              70              75              80

Gly Val Leu Tyr Phe Arg Thr His Leu Trp Val Glu Leu Ile Val Leu
            85              90              95

Phe Leu Phe Leu Tyr Arg Phe Leu Tyr Arg Ile Ala Glu Ile Gly Gln
            100             105             110

Leu Gln Thr Ala Val Ser Asp Gly Gly Ser Ala Ala Tyr Gly Ala Leu
        115             120             125

Phe Ala Gln Asp Pro Ala Thr Met Ile Gly Phe Phe Val Leu Ala Val
    130             135             140
```

```
Tyr Tyr Val Gly Phe Ser Phe Phe Val Leu Lys Lys Gly Arg Thr Glu
145                 150                 155                 160

Glu Lys Arg Ser Ala
                165
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<210> 118

<211> 2353

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1850)

<223>

<400> 118

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aaaggctgca cctaaacaag ccgcgcctaa aaaacaggat gccgttgcag ccaatatgcc     120

gggcggattc tcgaacaacg acattaatct gttggcccaa gcggtttacg gtgaagcgcg     180

cggagaaccg tatgacggcc aggttgccgt tgcagctgtt atattaaaca ggctcgatag     240

ccctacgttc ccgaatacgg tggcgggcgt tatctttgaa ccgcttgcat ttacagctgt     300

cgcggacgga cagatttata tgacgccgga tgaaacggcg aaaaaagccg ttcttgacgc     360

catcaacggc tgggatccat cagaaaatgc cacttactat tttaaccctg acacggccac     420

tagctcatgg atttggggca gacctcaaat taaaaggatc ggtaaacaca ttttctgtga     480

ataaaagcga ggtgctataa atg atc aga gga att tta atc gcc ctt tta ggt     533
                      Met Ile Arg Gly Ile Leu Ile Ala Leu Leu Gly
                       1               5                  10

gtc gcc atc gtc gga aca agc tat tgg ggc tat aaa gaa cat cag gag     581
Val Ala Ile Val Gly Thr Ser Tyr Trp Gly Tyr Lys Glu His Gln Glu
            15                  20                  25

aaa gac gcc gtt ttg ctt cat gcc gaa aac aac tat caa agg gca ttt     629
Lys Asp Ala Val Leu Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe
            30                  35                  40

cac gac tta act tat cag gtg gat cag ctg cat gat aaa atc ggg agc     677
His Asp Leu Thr Tyr Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser
        45                  50                  55

acg ctt gcg atg aac agc aaa aaa acg ctg tct ccc gct ttg gcg gaa     725
Thr Leu Ala Met Asn Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu
60                  65                  70                  75

gtc tgg aaa acg act tct gaa gcg cat aac aat gtc agc cag ctg ccg     773
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Page 181

```
Val Trp Lys Thr Thr Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro
             80              85              90

ctg acc tta atg ccg ttt aac aag acc gaa gag ttt ttg gca aag gtc    821
Leu Thr Leu Met Pro Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val
             95              100             105

gga gat ttc agc tac aaa gca gcc gtg cgc gat ctt gac aaa gag ccg    869
Gly Asp Phe Ser Tyr Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro
             110             115             120

ctc aat aaa aaa gag tac gct tct tta aat cag cta tat gaa aat tca    917
Leu Asn Lys Lys Glu Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser
             125             130             135

aag gat ata caa aat gaa ctg cgt aat gtc cag cat ttg att att gac    965
Lys Asp Ile Gln Asn Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp
140             145             150             155

aaa aat ttg aga tgg atg gat gta gaa ctt gcg ctc gcg tcc ggc caa   1013
Lys Asn Leu Arg Trp Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln
             160             165             170

aaa caa agc gac aat aag att att aat ggc ttt aaa acc gtt gaa aaa   1061
Lys Gln Ser Asp Asn Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys
             175             180             185

agc gca agt gca ttt tcg gat acg gat tta ggc gcg aca gag atg acg   1109
Ser Ala Ser Ala Phe Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr
             190             195             200

aac acg aaa aaa gag cag caa ggg tac gac cat tta caa ggc aaa aga   1157
Asn Thr Lys Lys Glu Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg
             205             210             215

ata acc gaa aaa gaa gcg cgc aag att gcc caa aaa ttc gcc cag gac   1205
Ile Thr Glu Lys Glu Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp
220             225             230             235

aaa aat tac aat atc aaa gta tcg aaa agc ggc aag aaa acg aac agg   1253
Lys Asn Tyr Asn Ile Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg
             240             245             250

gat gta tac agc atc agt atg cag gac cct gat caa aaa gcg gat att   1301
Asp Val Tyr Ser Ile Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile
             255             260             265

tat atg gac att acc gaa aaa ggc gga tat ccg gtt tat ctg att caa   1349
Tyr Met Asp Ile Thr Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln
             270             275             280

aac aaa aaa att aaa gat gaa aaa atc agc tta aac gat gcg tca aac   1397
Asn Lys Lys Ile Lys Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn
             285             290             295

aaa gcc ctt caa ttt ttg aaa aaa aac ggc tat aaa acg gaa gac ctg   1445
Lys Ala Leu Gln Phe Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu
300             305             310             315

aag atg gat gaa agc tcg caa tac gac ggc gtc ggg gtg ttt tca ttt   1493
Lys Met Asp Glu Ser Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe
             320             325             330

gtt ccg gtc cag gac gat gtc tgg ctc tat ccg gac agc atc cgc atc   1541
Val Pro Val Gln Asp Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile
             335             340             345

aag gtc gcg ctt gac gac ggc gag att acc ggg ttt aat gca aag gat   1589
```

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Lys Val Ala Leu Asp Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp
        350             355             360

ttc tta atc tcc cat aaa aaa aga gac ttg ccg aag ccc aaa cta acg    1637
Phe Leu Ile Ser His Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr
        365             370             375

cct gaa aaa gcg aaa gca agc ctg aat ccc aac gta aaa gtt cag gag    1685
Pro Glu Lys Ala Lys Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu
380             385             390             395

acg cgc ctt gct tta gtc acg aac gag ctt tcg caa gaa gtg ctc tgc    1733
Thr Arg Leu Ala Leu Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys
                400             405             410

tac gaa att ctc ggc acg att gaa aac gat aca ttc cgc atg ttc atc    1781
Tyr Glu Ile Leu Gly Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile
                415             420             425

aat gcc aat gac ggc acg gaa gag aag gtt cag aaa atg aaa agc gca    1829
Asn Ala Asn Asp Gly Thr Glu Glu Lys Val Gln Lys Met Lys Ser Ala
        430             435             440

gaa ccg ata tac aac gac ttg taaaaacgat agatcaaagg gaaaaggcga      1880
Glu Pro Ile Tyr Asn Asp Leu
        445             450

taacatgcct tttccttttt agcattcgga ataattcgcc ctaaacattt ccatactgaa   1940

catatgggcg gaacgtccgc cggtaaattg aaaatgcccg ggccataaa ttttccgggc   2000

agcggaggaa taatatgaaa acaatcgaac ggttattatt taagatactc gtcgtacaga   2060

cggtcatttt aatcagcgtg cagcttcttt ttcatttctc caaggctgag ccttatctgt   2120

caaaggtcgt gcagtatgaa ggcgtgaaca acatgaaaat cggcgaatgg atcgagacat   2180

ttaagccgta attcacgcta aaatctcccc tttttcgcct aatacatgat acaatcctat   2240

aaggagtacc agatagcaag gagaggaatt atggaaaaga aattatgcat tgcaatagac   2300

ggccctgcgg cagccggaaa aagcaccgtg gcgaaaatcg tggccagaaa aaa        2353
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<210> 119

<211> 450

<212> PRT

<213> Bacillus licheniformis

<400> 119

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Met Ile Arg Gly Ile Leu Ile Ala Leu Leu Gly Val Ala Ile Val Gly
1               5               10              15

Thr Ser Tyr Trp Gly Tyr Lys Glu His Gln Glu Lys Asp Ala Val Leu
            20              25              30

Leu His Ala Glu Asn Asn Tyr Gln Arg Ala Phe His Asp Leu Thr Tyr
        35              40              45
```

```
Gln Val Asp Gln Leu His Asp Lys Ile Gly Ser Thr Leu Ala Met Asn
    50              55                60

Ser Lys Lys Thr Leu Ser Pro Ala Leu Ala Glu Val Trp Lys Thr Thr
65              70              75                  80

Ser Glu Ala His Asn Asn Val Ser Gln Leu Pro Leu Thr Leu Met Pro
            85              90                  95

Phe Asn Lys Thr Glu Glu Phe Leu Ala Lys Val Gly Asp Phe Ser Tyr
        100             105             110

Lys Ala Ala Val Arg Asp Leu Asp Lys Glu Pro Leu Asn Lys Lys Glu
        115             120             125

Tyr Ala Ser Leu Asn Gln Leu Tyr Glu Asn Ser Lys Asp Ile Gln Asn
    130             135             140

Glu Leu Arg Asn Val Gln His Leu Ile Ile Asp Lys Asn Leu Arg Trp
145             150             155             160

Met Asp Val Glu Leu Ala Leu Ala Ser Gly Gln Lys Gln Ser Asp Asn
            165             170             175

Lys Ile Ile Asn Gly Phe Lys Thr Val Glu Lys Ser Ala Ser Ala Phe
        180             185             190

Ser Asp Thr Asp Leu Gly Ala Thr Glu Met Thr Asn Thr Lys Lys Glu
    195             200             205

Gln Gln Gly Tyr Asp His Leu Gln Gly Lys Arg Ile Thr Glu Lys Glu
    210             215             220

Ala Arg Lys Ile Ala Gln Lys Phe Ala Gln Asp Lys Asn Tyr Asn Ile
225             230             235             240

Lys Val Ser Lys Ser Gly Lys Lys Thr Asn Arg Asp Val Tyr Ser Ile
            245             250             255

Ser Met Gln Asp Pro Asp Gln Lys Ala Asp Ile Tyr Met Asp Ile Thr
            260             265             270

Glu Lys Gly Gly Tyr Pro Val Tyr Leu Ile Gln Asn Lys Lys Ile Lys
    275             280             285

Asp Glu Lys Ile Ser Leu Asn Asp Ala Ser Asn Lys Ala Leu Gln Phe
    290             295             300

Leu Lys Lys Asn Gly Tyr Lys Thr Glu Asp Leu Lys Met Asp Glu Ser
305             310             315             320
```

Page 184

```
Ser Gln Tyr Asp Gly Val Gly Val Phe Ser Phe Val Pro Val Gln Asp
            325             330                 335

Asp Val Trp Leu Tyr Pro Asp Ser Ile Arg Ile Lys Val Ala Leu Asp
            340                 345                 350

Asp Gly Glu Ile Thr Gly Phe Asn Ala Lys Asp Phe Leu Ile Ser His
            355                 360                 365

Lys Lys Arg Asp Leu Pro Lys Pro Lys Leu Thr Pro Glu Lys Ala Lys
    370                 375                 380

Ala Ser Leu Asn Pro Asn Val Lys Val Gln Glu Thr Arg Leu Ala Leu
385                 390                 395                 400

Val Thr Asn Glu Leu Ser Gln Glu Val Leu Cys Tyr Glu Ile Leu Gly
            405                 410                 415

Thr Ile Glu Asn Asp Thr Phe Arg Met Phe Ile Asn Ala Asn Asp Gly
            420                 425                 430

Thr Glu Glu Lys Val Gln Lys Met Lys Ser Ala Glu Pro Ile Tyr Asn
            435                 440                 445

Asp Leu
    450
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<210> 120

<211> 1355

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (249)..(1355)

<223>

<400> 120

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attccccctg atgtcatgat ggatcttccg agaattacga tgataggaag acttcacata     60
tatattgaaa accacagagg cttttgctt ttcagcgata cggaagtaag gctgatgctc     120
aaacagggc agtgcatcat tcaaggcaaa gactttgtca tcaaaacgat tttgcctgag     180
gaaattctgc ttgaaggcac gattgagctt gtccgctata tcgattcata agtcggggg      240
aaagaagc gtg aag aat aaa tgg ctt tct ttt ttt tca gga aag atc cag     290
         Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Ile Gln
         1               5                   10
```

```
ctt aag ata acg gga aaa ggg atc gaa cgg tta tta aat gaa tgc acc    338
Leu Lys Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr
15              20              25              30

agg cgc aac atc ccg atg ttt aat gta aag aaa aag aaa gac gcc gtc    386
Arg Arg Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys Asp Ala Val
            35              40              45

ttt ctt tat att ccg ctt tct gat gta cat gcc ttc cgg aag gtc atc    434
Phe Leu Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile
            50              55              60

aga ggc ttc gac tgc aag tgc agg ttc atc aaa cga aaa ggg ttt cct    482
Arg Gly Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro
        65              70              75

ttc ctc gtg cag aag tct aaa cgg aat agc ggc ttc act ttt gga gtt    530
Phe Leu Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val
        80              85              90

gct gca ttt ttt atc atc atg ttc cta ttg tcc aac atg ctt tgg aaa    578
Ala Ala Phe Phe Ile Ile Met Phe Leu Leu Ser Asn Met Leu Trp Lys
95              100             105             110

att gat att aca gga gcc aat cca gag aca gaa cat caa atc aga cag    626
Ile Asp Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Arg Gln
                115             120             125

caa ttg gat caa atc ggc gtc aaa aaa ggc cgc ttt cag ttt tca atg    674
Gln Leu Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met
                130             135             140

ctg acc ccg gaa aaa att cag cag gcg ctc aca aag cgg gtc gaa aac    722
Leu Thr Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn
        145             150             155

atc act tgg gtg ggc att gag tta aac ggt acc gcc ctt cac atg aaa    770
Ile Thr Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys
        160             165             170

gtc gtt gaa aag aat gaa cct gac aaa gaa aaa tat atc ggt ccg agg    818
Val Val Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg
175             180             185             190

cac atc gtc gcc aaa aaa ggg gcg acc atc tcg aaa atg ttc gtg gaa    866
His Ile Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Met Phe Val Glu
                195             200             205

aaa ggc gag ccg ctc gtc acg gtg aac cag cac gtt gaa aaa ggg caa    914
Lys Gly Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln
                210             215             220

atg ctc gtt tcc ggg ctg atc gga agc gaa gag gaa aag caa aaa gtc    962
Met Leu Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val
        225             230             235

gga gca aaa ggg aaa atc tat ggt gaa acc tgg tac aag tca aca gta    1010
Gly Ala Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val
        240             245             250

acg gtt cct ctt gag aca tca ttt gac gtt ttt acg ggt aaa gta agg    1058
Thr Val Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg
255             260             265             270

aca agt cac aag cta tcc ctc gga tca tta acc atg ccg atc tgg ggc    1106
Thr Ser His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly
                275             280             285
```

```
ttt tca ttt aaa aaa gaa gac ttc tcg cgc ccg aag acg gag acc gaa          1154
Phe Ser Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu
            290             295             300

aaa cac tcg ctg cat ttt ata aat ttt aag ctt cct gtc gct tat gaa          1202
Lys His Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu
            305             310             315

aag gag cat atg agg gag agc gaa caa atc aaa agg gtg tac tcg aaa          1250
Lys Glu His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys
            320             325             330

aaa gaa gca gtt ctt aga agg aat cga aat ggg aaa aag aga cat cag          1298
Lys Glu Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln
335             340             345             350

gac aaa aat cgg cag aga cgg gaa cat tat cag tgt aaa agt ttt gca          1346
Asp Lys Asn Arg Gln Arg Arg Glu His Tyr Gln Cys Lys Ser Phe Ala
            355             360             365

cac cac gag                                                              1355
His His Glu
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<210> 121

<211> 369

<212> PRT

<213> Bacillus licheniformis

<400> 121

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Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Ile Gln Leu Lys
1               5               10              15

Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr Arg Arg
            20              25              30

Asn Ile Pro Met Phe Asn Val Lys Lys Lys Asp Ala Val Phe Leu
            35              40              45

Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile Arg Gly
    50              55              60

Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro Phe Leu
65              70              75              80

Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val Ala Ala
                85              90              95

Phe Phe Ile Ile Met Phe Leu Leu Ser Asn Met Leu Trp Lys Ile Asp
            100             105             110

Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Arg Gln Gln Leu
            115             120             125
```

Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met Leu Thr
    130   135   140

Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn Ile Thr
145   150   155   160

Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys Val Val
                165   170   175

Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg His Ile
            180   185   190

Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Met Phe Val Glu Lys Gly
        195   200   205

Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln Met Leu
    210   215   220

Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val Gly Ala
225   230   235   240

Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val Thr Val
            245   250   255

Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg Thr Ser
            260   265   270

His Lys Leu Ser Leu Gly Ser Leu Thr Met Pro Ile Trp Gly Phe Ser
        275   280   285

Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu Lys His
    290   295   300

Ser Leu His Phe Ile Asn Phe Lys Leu Pro Val Ala Tyr Glu Lys Glu
305   310   315   320

His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys Lys Glu
                325   330   335

Ala Val Leu Arg Arg Asn Arg Asn Gly Lys Lys Arg His Gln Asp Lys
            340   345   350

Asn Arg Gln Arg Arg Glu His Tyr Gln Cys Lys Ser Phe Ala His His
            355   360   365

Glu

<210>   122

<211> 2120

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1625)

<223>

<400> 122
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ttaccaagat ctcggcttaa aggcgacaaa gctgacaaag gaaaaagcaa tcgacgaagg     120

cccgggctac acgagcattt ccttagaaaa gctgcctgat ttcgctggag attatatatt     180

tataggacct tgggaatcaa gcggagacga cagcgccgtg cttaatacat ccatttggaa     240

gaaccttggg gcggtcaaaa accaacatgt ctataaaatc gaccctgtcg gcttctattt     300

ttccgatccg atttcattag agggccagct cgaatttatt acagaaaact aacaaaata     360

gaagaacttc cgccttgtca ggcggaagtt tttttgcgc gcgaaaccgg ggtgaaccct     420

cattgaaaaa gcgattttca agtgcaagcc gggagagttt ttaaacgagc attcctcata     480

tgctattgtg ggagggatca ttg atg gca ttc atc aac atc aaa ccg gag tta     533
                         Leu Met Ala Phe Ile Asn Ile Lys Pro Glu Leu
                          1           5                   10

aag cag aat atg gaa aga ctg tct gac att ctg aac ata ccc gaa ccg     581
Lys Gln Asn Met Glu Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro
            15              20                  25

ctt tta atc agt gca aat gca aat gta tcc gcg gac gaa ctt tat ttt     629
Leu Leu Ile Ser Ala Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe
            30              35                  40

ccg gga gta tct ttt cat gca gga aaa aac gtt caa gca gca gaa aca     677
Pro Gly Val Ser Phe His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr
        45              50                  55

tat gaa cag ctg caa tta ttg gcg aat caa tac acg ttt gaa gat gaa     725
Tyr Glu Gln Leu Gln Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu
60              65                  70                  75

cag tgg ctg aca aaa aca gcc gtt tac gat tca gca gaa ctg aaa aag     773
Gln Trp Leu Thr Lys Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys
                80                  85                  90

gaa att ggc aga ttg acg gaa tgc ttt ccg ttt gtt act tcc cgt atc     821
Glu Ile Gly Arg Leu Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile
                95                  100                 105

atc ggc cgc tca agc atg ggc cag cct ata tat gaa ctg ctc ctt gga     869
Ile Gly Arg Ser Ser Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly
            110                 115                 120

gct gaa aat gcc gga aaa aga acg cat atg aat gcc tct ttt cat gcc     917
Ala Glu Asn Ala Gly Lys Arg Thr His Met Asn Ala Ser Phe His Ala
```

```
Ala Glu Asn Ala Gly Lys Arg Thr His Met Asn Ala Ser Phe His Ala
    125             130             135
```

```
aat gaa tgg atc acc act tct gtt ttg atg aaa tgg ctc aaa gaa tac.    965
Asn Glu Trp Ile Thr Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr
140             145             150             155
```

```
tgt tat cat tta tgt aca ggc cag acc gct tta ggt ttt tcg ccg ctc    1013
Cys Tyr His Leu Cys Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu
                160             165             170
```

```
gat att ttt tca tca aca aag ctt tcc gtc gtg ccg atc gtt aat ccc    1061
Asp Ile Phe Ser Ser Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro
            175             180             185
```

```
gac ggt gtt gac ctt gta ctt aac ggc ccc ggt cat ctt ggg atc gcg    1109
Asp Gly Val Asp Leu Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala
        190             195             200
```

```
aga gaa gcg ctg gat gag atg aac gag cat cag ccg gat ttc cgg gaa    1157
Arg Glu Ala Leu Asp Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu
    205             210             215
```

```
tgg aaa gcc aat ata aac gga gtg gat tta aat aat cag ttt ccg tct    1205
Trp Lys Ala Asn Ile Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser
220             225             230             235
```

```
ttc tgg gag atc gaa aaa caa aga aaa ccg cct aaa tcc cct tcc tac    1253
Phe Trp Glu Ile Glu Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr
            240             245             250
```

```
aga gac tac ccc gga gat gaa ccg ctg aca gaa ccg gaa gcg gca gcg    1301
Arg Asp Tyr Pro Gly Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala
            255             260             265
```

```
atg agg gat tta atc gca aac gag ccg cct gac cgg ctt gtg gcg ctt    1349
Met Arg Asp Leu Ile Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu
        270             275             280
```

```
cac aca cag ggg gag gaa att tat tgg gga tac aag gga ttg gag cct    1397
His Thr Gln Gly Glu Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro
        285             290             295
```

```
cct gaa tca gct gat gtg atc caa aca ttt gag cgc ctg agc ggt tat    1445
Pro Glu Ser Ala Asp Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr
300             305             310             315
```

```
aag ggc gtc aga tat ata gac agc tat gca gga ttt aga gat tgg ttt    1493
Lys Gly Val Arg Tyr Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe
            320             325             330
```

```
att cat tat tac gga aga gaa gga tat act gtt gaa ctt ggc aaa gga    1541
Ile His Tyr Tyr Gly Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly
            335             340             345
```

```
aaa aat cct tta ccg ctg aaa caa ttt gac gat ata tat tgt aaa agc    1589
Lys Asn Pro Leu Pro Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser
        350             355             360
```

```
aga gga ata ctt tgg gca tcc tgt ttt ttt gaa agc tgaaactttt         1635
Arg Gly Ile Leu Trp Ala Ser Cys Phe Phe Glu Ser
    365             370             375
```

```
cacggtgaaa atcgtaaatt agacagccaa acatttatgg agggagaatg gccggtttga   1695
```

```
gagtttcatt attgattatt gccgctctga tggccgtggc tgcggctggt tgcacgccgc   1755
```

```
agcatcaaga aggatcaaaa agcgttcatc atgaggagcc ggaagggaaa agagaaagcg   1815
```

```
gtgcagcagt aaaagataaa aaagtgatag cgctgaagga ccggcacttt gatgagacgg    1875

caggatggct tgataatgaa accgttatat acaccgcaac cgatccggtc ggaggaagtg    1935

aaatcaaatc atatgatata tttaaaggga cgggcaaaac gatctacaag acagatgaca    1995

ggctgatagc gtcggaagtc aacagtgaaa aaggcatgat tcttatccaa accgccggaa    2055

acggctctga aatgaagtta actttgctta atttacaggg gaaacagctg tttgcaaaaa    2115

aattt                                                               2120
```

<210> 123

<211> 375

<212> PRT

<213> Bacillus licheniformis

<400> 123

```
Leu Met Ala Phe Ile Asn Ile Lys Pro Glu Leu Lys Gln Asn Met Glu
1               5               10              15


Arg Leu Ser Asp Ile Leu Asn Ile Pro Glu Pro Leu Leu Ile Ser Ala
            20              25              30


Asn Ala Asn Val Ser Ala Asp Glu Leu Tyr Phe Pro Gly Val Ser Phe
        35              40              45


His Ala Gly Lys Asn Val Gln Ala Ala Glu Thr Tyr Glu Gln Leu Gln
    50              55              60


Leu Leu Ala Asn Gln Tyr Thr Phe Glu Asp Glu Gln Trp Leu Thr Lys
65              70              75              80


Thr Ala Val Tyr Asp Ser Ala Glu Leu Lys Lys Glu Ile Gly Arg Leu
                85              90              95


Thr Glu Cys Phe Pro Phe Val Thr Ser Arg Ile Ile Gly Arg Ser Ser
            100             105             110


Met Gly Gln Pro Ile Tyr Glu Leu Leu Leu Gly Ala Glu Asn Ala Gly
        115             120             125


Lys Arg Thr His Met Asn Ala Ser Phe His Ala Asn Glu Trp Ile Thr
    130             135             140


Thr Ser Val Leu Met Lys Trp Leu Lys Glu Tyr Cys Tyr His Leu Cys
145             150             155             160


Thr Gly Gln Thr Ala Leu Gly Phe Ser Pro Leu Asp Ile Phe Ser Ser
                165             170             175
```

Page 191

Thr Lys Leu Ser Val Val Pro Ile Val Asn Pro Asp Gly Val Asp Leu
            180   185   190

Val Leu Asn Gly Pro Gly His Leu Gly Ile Ala Arg Glu Ala Leu Asp
            195   200   205

Glu Met Asn Glu His Gln Pro Asp Phe Arg Glu Trp Lys Ala Asn Ile
    210   215   220

Asn Gly Val Asp Leu Asn Asn Gln Phe Pro Ser Phe Trp Glu Ile Glu
225   230   235   240

Lys Gln Arg Lys Pro Pro Lys Ser Pro Ser Tyr Arg Asp Tyr Pro Gly
            245   250   255

Asp Glu Pro Leu Thr Glu Pro Glu Ala Ala Ala Met Arg Asp Leu Ile
            260   265   270

Ala Asn Glu Pro Pro Asp Arg Leu Val Ala Leu His Thr Gln Gly Glu
            275   280   285

Glu Ile Tyr Trp Gly Tyr Lys Gly Leu Glu Pro Pro Glu Ser Ala Asp
    290   295   300

Val Ile Gln Thr Phe Glu Arg Leu Ser Gly Tyr Lys Gly Val Arg Tyr
305   310   315   320

Ile Asp Ser Tyr Ala Gly Phe Arg Asp Trp Phe Ile His Tyr Tyr Gly
            325   330   335

Arg Glu Gly Tyr Thr Val Glu Leu Gly Lys Gly Lys Asn Pro Leu Pro
            340   345   350

Leu Lys Gln Phe Asp Asp Ile Tyr Cys Lys Ser Arg Gly Ile Leu Trp
        355   360   365

Ala Ser Cys Phe Phe Glu Ser
        370   375

<210>   124

<211>   1597

<212>   DNA

<213>   Bacillus licheniformis

<220>

<221>   CDS

<222> (342)..(1094)

<223>

<400> 124

```
cctttttttat tttcctaaat tttcgaaaag ccagttaatt tatcccatat atcagaagga      60

aaagcgatgg tcatctcaaa actgtaacca attattttct tgatagtgtg gctgcgacta     120

ttatgcgctg attgtttacg gtgcttgctt tttataccat tggttcattt gaccggaatc     180

gtgttttgat tgcaggaatt tttgttactg tttgtgaaaa aacagcagaa gaaaaacagc     240

ggaaaactcg cgtcttaggg cggatttcca aaaaaatgtc gtaaattcga tgcatcaatt     300

tgatgaaatc gcccggccat gcggtataat agattttgtg a atg aaa gat tca atg     356
                                             Met Lys Asp Ser Met
                                             1               5
```

```
ttg aaa gag agt ggt tac atc atg ggc cgt aaa tgg aac aat ata aaa      404
Leu Lys Glu Ser Gly Tyr Ile Met Gly Arg Lys Trp Asn Asn Ile Lys
            10                  15                  20
```

```
gag aag aaa gcg tcc aag gat gcg aat acg agc cga atc tac gcg aag      452
Glu Lys Lys Ala Ser Lys Asp Ala Asn Thr Ser Arg Ile Tyr Ala Lys
        25                  30                  35
```

```
ttc ggc cgc gaa atc tat gtg gcg gca aag cag gga gag ccc gat ccc      500
Phe Gly Arg Glu Ile Tyr Val Ala Ala Lys Gln Gly Glu Pro Asp Pro
        40                  45                  50
```

```
gaa ctg aac cag aac ctg aaa ttc gtg ctt gag cgc gcc aaa aca tac      548
Glu Leu Asn Gln Asn Leu Lys Phe Val Leu Glu Arg Ala Lys Thr Tyr
    55                  60                  65
```

```
aat gtc ccg aaa gcg att att gag cgg gcg atc gaa aaa gcg aag ggc      596
Asn Val Pro Lys Ala Ile Ile Glu Arg Ala Ile Glu Lys Ala Lys Gly
70                  75                  80                  85
```

```
ggc tct gag gaa aat tac gac gag ctg cgc tat gaa ggc ttc ggt ccg      644
Gly Ser Glu Glu Asn Tyr Asp Glu Leu Arg Tyr Glu Gly Phe Gly Pro
                90                  95                  100
```

```
aac gga gcg atg gtg atc gtt gac gcg ttg aca aac aac gtc aac cgc      692
Asn Gly Ala Met Val Ile Val Asp Ala Leu Thr Asn Asn Val Asn Arg
            105                 110                 115
```

```
acg gct gcc gat gtg cgc tcc aca ttt ggc aaa aac ggc gga aac atg      740
Thr Ala Ala Asp Val Arg Ser Thr Phe Gly Lys Asn Gly Gly Asn Met
            120                 125                 130
```

```
gga gtg agc gga tct gtc gct tac atg ttt gat ccg acg gcc gtc atc      788
Gly Val Ser Gly Ser Val Ala Tyr Met Phe Asp Pro Thr Ala Val Ile
        135                 140                 145
```

```
ggc ttt gaa ggc aaa acg gct gat gaa acg ctc gaa tta ttg atg gaa      836
Gly Phe Glu Gly Lys Thr Ala Asp Glu Thr Leu Glu Leu Leu Met Glu
150                 155                 160                 165
```

```
gcg gat atc gat gtc cgt gat att tta gag gaa gac gat gca gtg atc      884
Ala Asp Ile Asp Val Arg Asp Ile Leu Glu Glu Asp Asp Ala Val Ile
                170                 175                 180
```

```
gtc tat gcc gag ccc gat cag ttc cac gcc gta cag gag gcg ctg caa      932
Val Tyr Ala Glu Pro Asp Gln Phe His Ala Val Gln Glu Ala Leu Gln
            185                 190                 195
```

```
aac gcc ggc att act gag ttc acg gtg gcc gag ctg acg atg ctc gcg        980
Asn Ala Gly Ile Thr Glu Phe Thr Val Ala Glu Leu Thr Met Leu Ala
        200                 205                 210

caa aat gac gtc gcc ctt cca gag gac gcg cgc gca cag ttt gaa aag       1028
Gln Asn Asp Val Ala Leu Pro Glu Asp Ala Arg Ala Gln Phe Glu Lys
        215                 220                 225

ctg att gac gcg ctg gaa gat ctg gaa gac gtt cag caa gtt tac cat       1076
Leu Ile Asp Ala Leu Glu Asp Leu Glu Asp Val Gln Gln Val Tyr His
230                 235                 240                 245

aat gtc gat tta ggg gcg taaaaagagg ccctgaaaaa atcgggaaag             1124
Asn Val Asp Leu Gly Ala
                250

aaaagataga tgaacaggag gacgacctgt tttgtctatc ttttttatt gtaaagttaa     1184

cttgacattt tattttttg ttaagtatac tttacgtata gtgaacttta cattcccaat     1244

ggaggaaaga tgaaaacgtt aataaaggaa aagcgcactt cgctgaacat gacacaagaa     1304

gaactggcta aaaggcttaa tgtgtcgagg caaacggtga tttcccttga aaagggaaaa     1364

tataaacctt cactcgttct ggcgcataaa ctggctcaaa tttttgaatg tctgattgaa     1424

gatttattta ttttgaggg ggatgaaaat attgactgaa acgatgacaa acatactgat      1484

cgctttagcg ggcttagaat aggcgtgctc gggatcgcaa ttgtttacaa agtaaacaga     1544

cgaattggaa aaaagagag gctgttcgat gagcgccagc agaagattag cta            1597
```

<210> 125

<211> 251

<212> PRT

<213> Bacillus licheniformis

<400> 125

```
Met Lys Asp Ser Met Leu Lys Glu Ser Gly Tyr Ile Met Gly Arg Lys
1               5                   10                  15

Trp Asn Asn Ile Lys Glu Lys Lys Ala Ser Lys Asp Ala Asn Thr Ser
            20                  25                  30

Arg Ile Tyr Ala Lys Phe Gly Arg Glu Ile Tyr Val Ala Ala Lys Gln
            35                  40                  45

Gly Glu Pro Asp Pro Glu Leu Asn Gln Asn Leu Lys Phe Val Leu Glu
    50                  55                  60

Arg Ala Lys Thr Tyr Asn Val Pro Lys Ala Ile Ile Glu Arg Ala Ile
65                  70                  75                  80

Glu Lys Ala Lys Gly Gly Ser Glu Glu Asn Tyr Asp Glu Leu Arg Tyr
                85                  90                  95
```

```
Glu Gly Phe Gly Pro Asn Gly Ala Met Val Ile Val Asp Ala Leu Thr
            100             105                 110

Asn Asn Val Asn Arg Thr Ala Ala Asp Val Arg Ser Thr Phe Gly Lys
        115             120                 125

Asn Gly Gly Asn Met Gly Val Ser Gly Ser Val Ala Tyr Met Phe Asp
    130             135                 140

Pro Thr Ala Val Ile Gly Phe Glu Gly Lys Thr Ala Asp Glu Thr Leu
145             150             155                 160

Glu Leu Leu Met Glu Ala Asp Ile Asp Val Arg Asp Ile Leu Glu Glu
            165             170                 175

Asp Asp Ala Val Ile Val Tyr Ala Glu Pro Asp Gln Phe His Ala Val
            180             185                 190

Gln Glu Ala Leu Gln Asn Ala Gly Ile Thr Glu Phe Thr Val Ala Glu
        195             200                 205

Leu Thr Met Leu Ala Gln Asn Asp Val Ala Leu Pro Glu Asp Ala Arg
    210             215                 220

Ala Gln Phe Glu Lys Leu Ile Asp Ala Leu Glu Asp Leu Glu Asp Val
225             230             235                 240

Gln Gln Val Tyr His Asn Val Asp Leu Gly Ala
            245             250
```

<210> 126

<211> 1888

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (3)..(1385)

<223>

<400> 126

```
ag aag gat gct gcg cgc cgg aat gtc gat gat gct cgt aca ggc atc     47
   Lys Asp Ala Ala Arg Arg Asn Val Asp Asp Ala Arg Thr Gly Ile
   1           5               10                  15

att gct ttc tcc att cta tat ttg tcc gcc ccg ttt ttt gca gag atg    95
```

Page 195

```
Ile Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met
            20                  25                  30

gcc ctt ggc gga aca gaa aac aac ggg ctg acg ctt gaa cat gtc gtg    143
Ala Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val
            35                  40                  45

tat gtc att cgc atg gtc agt ctc gcg cta ctg gtt gtg ccg atc ttg    191
Tyr Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu
            50                  55                  60

gcg ctg atc aga ggc ttt ttc caa ggt cac cag atg atg ggg ccg aca    239
Ala Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr
    65                  70                  75

gcc gtt tca cag gta gtt gaa caa att gcc aga atc gtc ttt cta tta    287
Ala Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu
80              85                  90                  95

acg gcc act tac ttg gtg atc aaa gta tta aac ggc ggg ctt gtc gtc    335
Thr Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val
                100                 105                 110

gct gtc ggc tat gcg act ttt gcg gct ttg atc gga gcg ttc gcc gga    383
Ala Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly
            115                 120                 125

ctg ttc act ctt tac ttt tcc tgg cag aaa aga aaa ggg gcg ctc ctg    431
Leu Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu
            130                 135                 140

gcg ctg aag ccg aac ctt gtt cct tca gcc gat att acg tac cgg caa    479
Ala Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln
    145                 150                 155

atg ttt aaa gag ctg ttc agc tat gcc gcc cct tat gtc ttt gtc ggg    527
Met Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly
160                 165                 170                 175

ctg gcg ata ccg ctt tac cag tac att gat acg aat acg ttt aat aaa    575
Leu Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys
                180                 185                 190

gcg atg att gca gcc ggc tat caa aac atc agc cag gat ttg atg gcg    623
Ala Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala
            195                 200                 205

atc gtg acg ctg tac gtg cca aag ctt gtg atg att ccg gta tct ctc    671
Ile Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu
            210                 215                 220

gcg acg gca ttc ggg ctg aca ttg att ccg gcg gtg act gaa aac ttt    719
Ala Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe
    225                 230                 235

acc aac aaa gat ttc cct gct tta aac aaa cag att gat cag gcg atg    767
Thr Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met
240                 245                 250                 255

cag atc att ctc ttc atc gtt ctt ccg gca tca gtc ggt atg gct ctt    815
Gln Ile Ile Leu Phe Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu
                260                 265                 270

ttg tcg ggg ccg gtt tac acg ttc ttt tac ggc tcg gaa agc ctg ctc    863
Leu Ser Gly Pro Val Tyr Thr Phe Phe Tyr Gly Ser Glu Ser Leu Leu
            275                 280                 285

cct gac atg gga cga gat att ttg ttc tgg tac gcg cct gtg gcg ctg    911
```

Page 196

```
Pro Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu
        290              295              300

tta ttc tcg ctc ttc acc gtc aac gct gca att ttg cag ggg gtg aac    959
Leu Phe Ser Leu Phe Thr Val Asn Ala Ala Ile Leu Gln Gly Val Asn
        305              310              315

aag cag aaa ttt gcg gtt gtc agc ttg atg atc ggg att gtg atc aaa   1007
Lys Gln Lys Phe Ala Val Val Ser Leu Met Ile Gly Ile Val Ile Lys
320              325              330              335

atc gcg ctt aac gtt ccg ctc atc aag ctg ctt caa ggc agc ggg tcg   1055
Ile Ala Leu Asn Val Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser
            340              345              350

att ttg gca acg gcg ctc ggc tat tca gct tca ctc cta tac gga ttt   1103
Ile Leu Ala Thr Ala Leu Gly Tyr Ser Ala Ser Leu Leu Tyr Gly Phe
            355              360              365

atc atg att aaa cgc cat gcc ggc tat tcg tat cgc aaa ctg ttt aaa   1151
Ile Met Ile Lys Arg His Ala Gly Tyr Ser Tyr Arg Lys Leu Phe Lys
        370              375              380

cgg ttt ttg ctg atg ctg atc ctg acg gcg gtc atg ggc atc att ttg   1199
Arg Phe Leu Leu Met Leu Ile Leu Thr Ala Val Met Gly Ile Ile Leu
        385              390              395

ctg ctt gtc cag gcg ctt cta agt att ttt att tca tac gaa ggc ggg   1247
Leu Leu Val Gln Ala Leu Leu Ser Ile Phe Ile Ser Tyr Glu Gly Gly
400              405              410              415

cag atc agg tct gct gtc gtc att ttc atc aca acc gca gtg ggc ggg   1295
Gln Ile Arg Ser Ala Val Val Ile Phe Ile Thr Thr Ala Val Gly Gly
            420              425              430

tca gtt tat ctg tac ttg gct tac cgt gtg aaa ctg ctc gaa aaa atc   1343
Ser Val Tyr Leu Tyr Leu Ala Tyr Arg Val Lys Leu Leu Glu Lys Ile
            435              440              445

ttc ggt cag cga ttg aat cgc ttt ttc aaa aga aag gcc tcc          1385
Phe Gly Gln Arg Leu Asn Arg Phe Phe Lys Arg Lys Ala Ser
            450              455              460

taaaaagggc ttttcttttt atgtaaaaaa aggggtgtct tcatgagatt ggataaactg   1445

ttgtcaaaca gcggctatgg ttcgagaaaa gaagtcaaaa aaatgctgaa aaacggcgcg   1505

gtgcgcgtca atgatcaatt agtcaaagac gccaaaaagc acgttgaccc ggaatcagac   1565

gacatcacgg tatacggggc acccgtcatg taccgggaat ttatttactt aatgatgaac   1625

aagccgcaag gagtgctgtc agcaacagaa gacagccggc aggaaacggt tgtcgatttg   1685

ctcgacccgg agctgctgag gtttgagccg tttcctgtcg gaaggcttga caaggatact   1745

gagggactgc tgcttctgac gaatgacgga cagttggcac accagctttt atctccgaaa   1805

aaacacgtac ctaaaacgta tgaagtccat gtcaataagc cgattgatca agcggcactt   1865

gatcagcttg aaaaaggggt cga                                         1888
```

<210> 127

<211> 461

<212> PRT

<213> Bacillus licheniformis

<400> 127

Lys Asp Ala Ala Arg Arg Asn Val Asp Asp Ala Arg Thr Gly Ile Ile
1   5   10   15

Ala Phe Ser Ile Leu Tyr Leu Ser Ala Pro Phe Phe Ala Glu Met Ala
            20   25   30

Leu Gly Gly Thr Glu Asn Asn Gly Leu Thr Leu Glu His Val Val Tyr
        35   40   45

Val Ile Arg Met Val Ser Leu Ala Leu Leu Val Val Pro Ile Leu Ala
    50   55   60

Leu Ile Arg Gly Phe Phe Gln Gly His Gln Met Met Gly Pro Thr Ala
65   70   75   80

Val Ser Gln Val Val Glu Gln Ile Ala Arg Ile Val Phe Leu Leu Thr
                85   90   95

Ala Thr Tyr Leu Val Ile Lys Val Leu Asn Gly Gly Leu Val Val Ala
            100   105   110

Val Gly Tyr Ala Thr Phe Ala Ala Leu Ile Gly Ala Phe Ala Gly Leu
        115   120   125

Phe Thr Leu Tyr Phe Ser Trp Gln Lys Arg Lys Gly Ala Leu Leu Ala
    130   135   140

Leu Lys Pro Asn Leu Val Pro Ser Ala Asp Ile Thr Tyr Arg Gln Met
145   150   155   160

Phe Lys Glu Leu Phe Ser Tyr Ala Ala Pro Tyr Val Phe Val Gly Leu
                165   170   175

Ala Ile Pro Leu Tyr Gln Tyr Ile Asp Thr Asn Thr Phe Asn Lys Ala
            180   185   190

Met Ile Ala Ala Gly Tyr Gln Asn Ile Ser Gln Asp Leu Met Ala Ile
        195   200   205

Val Thr Leu Tyr Val Pro Lys Leu Val Met Ile Pro Val Ser Leu Ala
    210   215   220

Thr Ala Phe Gly Leu Thr Leu Ile Pro Ala Val Thr Glu Asn Phe Thr
225   230   235   240

Asn Lys Asp Phe Pro Ala Leu Asn Lys Gln Ile Asp Gln Ala Met Gln
                245   250   255

Page 198

Ile Ile Leu Phe Ile Val Leu Pro Ala Ser Val Gly Met Ala Leu Leu
    260   265   270

Ser Gly Pro Val Tyr Thr Phe Phe Tyr Gly Ser Glu Ser Leu Leu Pro
    275   280   285

Asp Met Gly Arg Asp Ile Leu Phe Trp Tyr Ala Pro Val Ala Leu Leu
    290   295   300

Phe Ser Leu Phe Thr Val Asn Ala Ala Ile Leu Gln Gly Val Asn Lys
305   310   315   320

Gln Lys Phe Ala Val Val Ser Leu Met Ile Gly Ile Val Ile Lys Ile
                325   330   335

Ala Leu Asn Val Pro Leu Ile Lys Leu Leu Gln Gly Ser Gly Ser Ile
            340   345   350

Leu Ala Thr Ala Leu Gly Tyr Ser Ala Ser Leu Leu Tyr Gly Phe Ile
        355   360   365

Met Ile Lys Arg His Ala Gly Tyr Ser Tyr Arg Lys Leu Phe Lys Arg
    370   375   380

Phe Leu Leu Met Leu Ile Leu Thr Ala Val Met Gly Ile Ile Leu Leu
385   390   395   400

Leu Val Gln Ala Leu Leu Ser Ile Phe Ile Ser Tyr Glu Gly Gly Gln
            405   410   415

Ile Arg Ser Ala Val Val Ile Phe Ile Thr Thr Ala Val Gly Gly Ser
            420   425   430

Val Tyr Leu Tyr Leu Ala Tyr Arg Val Lys Leu Leu Glu Lys Ile Phe
        435   440   445

Gly Gln Arg Leu Asn Arg Phe Phe Lys Arg Lys Ala Ser
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<211>   1852

<212>   DNA

<213>   Bacillus 1icheniformis

<220>

<221>   CDS

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<223>

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acgcgctgtc gcccgccttt cggttctcag cgagctctgc cttccgcttg tgaaaaaaga     180

cggtttattc gtagcattaa aagccgcttc ggctgatgaa gaaattgaaa cgggcaaaaa     240

agccatcaaa acgcttggag gcaaaattga aaccgtacat tcttttcagc tgccaataga     300

agaaagcgaa agaaacatca ttgtcatcaa aaaacaatcg cagacaccga gaaatttcc      360

aagaaagcct ggaacaccta ataaatctcc tattgaaggt taaattattc gttttcttca     420

aatttcgtga tgtcacagaa ggaaaattca tgagaaaata gaattataaa aatggcagtg     480
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                      Met Lys His Ser Phe Ser Arg Leu Phe Gly Leu
                       1               5                      10

ggc gac aag gaa gaa gaa gca gag att gct gaa cat gat acg aat aaa         581
Gly Asp Lys Glu Glu Glu Ala Glu Ile Ala Glu His Asp Thr Asn Lys
                 15                  20                  25

gaa gaa att caa gag att cca gta ggc gat ata att cct aac cgt ttt         629
Glu Glu Ile Gln Glu Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe
             30                  35                  40

cag ccg cgc acc att ttc tca gaa gaa aaa att aaa gaa tta gct gca         677
Gln Pro Arg Thr Ile Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala
         45                  50                  55

acc att cat aca cac ggc att atc cag ccg att gtc gtc aga aaa aca         725
Thr Ile His Thr His Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr
60                  65                  70                  75

gag cgg gaa ggc caa tat gaa ctc ata gcc gga gag cgg cgc tgg cgg         773
Glu Arg Glu Gly Gln Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg
                 80                  85                  90

gcg gtt caa acg ctc gat tgg gag aag gtt ccc gct att att aag gat         821
Ala Val Gln Thr Leu Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp
             95                 100                 105

ttt tca gat aca gag acc gct tct gtc gct ctt atc gaa aac ctt cag         869
Phe Ser Asp Thr Glu Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln
         110                 115                 120

agg gaa gaa tta tct tcg att gaa gag gcg cat gct tat gca agg ctt         917
Arg Glu Glu Leu Ser Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu
         125                 130                 135

tta gag ctt cac gat ttg acg cag gaa gcc ctt gca caa agg ctt gga         965
Leu Glu Leu His Asp Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly
140                 145                 150                 155

aag ggc cag tca aca atc gcc aat aag ctc aga ctg tta aag ctt ccg        1013
Lys Gly Gln Ser Thr Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro
                 160                 165                 170

gaa gag gtg cag gaa gcg atc ttg aaa aaa gaa att tca gag cgc cac        1061
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Page 200

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     Glu Glu Val Gln Glu Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His
                 175             180             185

     gca aga gcg ctc ata ccg ttg aaa cag ccc gac ctt cag gtc aag ctg      1109
     Ala Arg Ala Leu Ile Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu
                 190             195             200

     ctg cat gaa gtc att gaa aag agt tta aat gta aaa caa acc gaa gac      1157
     Leu His Glu Val Ile Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp
                 205             210             215

     cgt gtc gtc aaa atg ctt gag cag gat aaa cgc aag cct aaa cca aag      1205
     Arg Val Val Lys Met Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys
     220             225             230             235

     aga aaa gcg tac agc agg gac gcg aga atc gcg atg aat acg att cgc      1253
     Arg Lys Ala Tyr Ser Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg
                 240             245             250

     cag tcc tta tca atg gtg gaa gac agc ggc gtc aaa ctg aat acg gaa      1301
     Gln Ser Leu Ser Met Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu
                 255             260             265

     gaa gag gaa ttt gaa gaa tat att cag ttt acg att cga ata ccg aaa      1349
     Glu Glu Glu Phe Glu Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys
                 270             275             280

     taaaagctcc ctatagagct tttatttttt taggcaaaat atctatgggg gagcgtctat      1409

     ggaatattat cgacaatatc attcattgct tttttcgatt gcttaccgta tgctcgggtc      1469

     ttttcaagat gcagaggaca tcatccaaga attgttcgca gaccttcagg aaaaagatat      1529

     cggtcaaatt gaccatattc aagcatattt aacgaaatca atcacaaacc gctgcataaa      1589

     tgaactgcag tctgcccgca agaagcggga ggtatatatc ggggaatggc ttccggaacc      1649

     gcaggtggcg ctttcagctc aaatcccggc tgagtacgtt gaagagaaag aaaaggtatc      1709

     ctatgctttt ctggtagtta tgagccgatt aaatcctgta gaaagagccg ttttgatgtt      1769

     tagagaagta tttggatatc attacaagga aatttcgtcc attatcggga agtcggaagc      1829

     gaactgtcgt caaatccaca gcc                                            1852
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     Ile Pro Val Gly Asp Ile Ile Pro Asn Arg Phe Gln Pro Arg Thr Ile
                 35              40              45
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Phe Ser Glu Glu Lys Ile Lys Glu Leu Ala Ala Thr Ile His Thr His
    50   55   60

Gly Ile Ile Gln Pro Ile Val Val Arg Lys Thr Glu Arg Glu Gly Gln
65   70   75   80

Tyr Glu Leu Ile Ala Gly Glu Arg Arg Trp Arg Ala Val Gln Thr Leu
                85   90   95

Asp Trp Glu Lys Val Pro Ala Ile Ile Lys Asp Phe Ser Asp Thr Glu
            100   105   110

Thr Ala Ser Val Ala Leu Ile Glu Asn Leu Gln Arg Glu Glu Leu Ser
        115   120   125

Ser Ile Glu Glu Ala His Ala Tyr Ala Arg Leu Leu Glu Leu His Asp
    130   135   140

Leu Thr Gln Glu Ala Leu Ala Gln Arg Leu Gly Lys Gly Gln Ser Thr
145   150   155   160

Ile Ala Asn Lys Leu Arg Leu Leu Lys Leu Pro Glu Glu Val Gln Glu
            165   170   175

Ala Ile Leu Lys Lys Glu Ile Ser Glu Arg His Ala Arg Ala Leu Ile
            180   185   190

Pro Leu Lys Gln Pro Asp Leu Gln Val Lys Leu Leu His Glu Val Ile
        195   200   205

Glu Lys Ser Leu Asn Val Lys Gln Thr Glu Asp Arg Val Val Lys Met
    210   215   220

Leu Glu Gln Asp Lys Arg Lys Pro Lys Pro Lys Arg Lys Ala Tyr Ser
225   230   235   240

Arg Asp Ala Arg Ile Ala Met Asn Thr Ile Arg Gln Ser Leu Ser Met
            245   250   255

Val Glu Asp Ser Gly Val Lys Leu Asn Thr Glu Glu Glu Glu Phe Glu
            260   265   270

Glu Tyr Ile Gln Phe Thr Ile Arg Ile Pro Lys
    275   280